

Swope, Sheridan

From: Swope, Sheridan
Sent: Thursday, February 09, 2006 3:04 PM
To: Chan, Christina
Subject: FW: 08/817,997_10/714,755

Chris, May I have this rushed?--Not enough hits collected in the A_Geneseq database.

From 08/817,997, please search :

SID 2, residues 36-229, against the A_Geneseq (.rag) database only.
**Collect the top 250 hits.

Note: this sequence begins with: (N-terminus)-Gln-Leu-Gly-Ala-Ile-
and ends with: -Asp-Arg-Ile-Arg-Ala-(C-terminus)

Please let me know if you have any questions.

Thanks,
Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

See Claim 45

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Tuesday, January 31, 2006 10:25 AM
To: Swope, Sheridan
Subject: RE: 08/817,997_10/714,755

CRFA - SEQUENCE MOVED TO PUBLIC DATABASE. Your request is in. maude

-----Original Message-----

From: Swope, Sheridan
Sent: Monday, January 30, 2006 9:23 PM
To: STIC-Biotech/ChemLib
Subject: 08/817,997_10/714,755

From 08/817,997, please search and interference search:

SID 2, residues 36-229, against the NT and AA data bases.

Note: this sequence begins with: (N-terminus)-Gln-Leu-Gly-Ala-Ile-
and ends with: -Asp-Arg-Ile-Arg-Ala-(C-terminus)

Please let me know if you have any questions.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
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STIC-Biotech/ChemLib

From: Swope, Sheridan
Sent: Monday, January 30, 2006 9:23 PM
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SID 2, residues 36-229, against the NT and AA data bases.

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and ends with: -Asp-Arg-Ile-Arg-Ala-(C-terminus)

Please let me know if you have any questions.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 178059

TO: Sheridan Swope
Location: rem/2B71/3C70
Art Unit: 1656
Wednesday, February 08, 2006
Case Serial Number: 08/817997

From: Kristine
Location: Biotech-Chem Library
REM-1B69
Phone: (571)272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner Swope,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2006, 04:48:19 ; Search time 199 Seconds
(without alignments)
428.339 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229
Perfect score: 996
Sequence: 1 QLGAIENGLESGSANACPD.....SYTIARGEARFLDRIRA 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 996 | 100.0 | 246 | 2 | AAR95051 H. insole |
| 2 | 991 | 99.5 | 194 | 5 | AAM48435 Wild-type |
| 3 | 991 | 99.5 | 194 | 6 | Aae34646 Humicola |
| 4 | 988 | 99.2 | 194 | 3 | AAB13715 H. insole |
| 5 | 987 | 99.1 | 194 | 3 | AAB13706 H. insole |
| 6 | 987 | 99.1 | 194 | 5 | ABB76837 Mutant Hu |
| 7 | 987 | 99.1 | 194 | 5 | ABB76844 Mutant Hu |
| 8 | 987 | 99.1 | 194 | 5 | ABB76838 Mutant Hu |
| 9 | 987 | 99.1 | 194 | 6 | Aae34652 Humicola |
| 10 | 985 | 98.9 | 194 | 3 | AAB13707 H. insole |
| 11 | 985 | 98.9 | 194 | 5 | ABB76839 Mutant Hu |
| 12 | 985 | 98.9 | 194 | 6 | Aae34653 Humicola |
| 13 | 984 | 98.8 | 194 | 3 | AAB13703 H. insole |
| 14 | 984 | 98.8 | 194 | 6 | Aae34649 Humicola |
| 15 | 983 | 98.7 | 194 | 3 | AAB13704 H. insole |
| 16 | 983 | 98.7 | 194 | 5 | ABB76845 Mutant Hu |
| 17 | 983 | 98.7 | 194 | 6 | Aae34650 Humicola |
| 18 | 982 | 98.6 | 194 | 3 | AAB13705 H. insole |
| 19 | 982 | 98.6 | 194 | 3 | AAB13711 H. insole |
| 20 | 982 | 98.6 | 194 | 5 | ABB76829 Mutant Hu |
| 21 | 982 | 98.6 | 194 | 6 | Aae34651 Humicola |
| 22 | 982 | 98.6 | 194 | 6 | Aae34657 Humicola |
| 23 | 981 | 98.5 | 194 | 3 | AAB13710 H. insole |
| 24 | 981 | 98.5 | 194 | 5 | ABB76834 Mutant Hu |

| | | | | | |
|----|-----|------|-----|---|--------------------|
| 25 | 981 | 98.5 | 194 | 6 | Aae34656 Humicola |
| 26 | 980 | 98.4 | 194 | 5 | ABB76831 Mutant Hu |
| 27 | 979 | 98.3 | 194 | 3 | AAB13717 H. insole |
| 28 | 977 | 98.1 | 194 | 3 | AAB13716 H. insole |
| 29 | 976 | 98.0 | 194 | 3 | AAB13709 H. insole |
| 30 | 976 | 98.0 | 194 | 5 | ABB76830 Mutant Hu |
| 31 | 976 | 98.0 | 194 | 6 | Aae34655 Humicola |
| 32 | 975 | 97.9 | 194 | 5 | ABB76836 Mutant Hu |
| 33 | 975 | 97.9 | 194 | 5 | ABB76846 Mutant Hu |
| 34 | 975 | 97.9 | 194 | 5 | ABB76843 Mutant Hu |
| 35 | 974 | 97.8 | 194 | 3 | AAB13708 H. insole |
| 36 | 974 | 97.8 | 194 | 6 | Aae34654 Humicola |
| 37 | 970 | 97.4 | 194 | 5 | ABB76832 Mutant Hu |
| 38 | 970 | 97.4 | 194 | 5 | ABB76828 Mutant Hu |
| 39 | 969 | 97.3 | 194 | 3 | AAB13718 H. insole |
| 40 | 969 | 97.3 | 194 | 5 | ABB76857 Mutant Hu |
| 41 | 969 | 97.3 | 194 | 6 | Aae34660 Humicola |
| 42 | 968 | 97.2 | 194 | 5 | ABB76835 Mutant Hu |
| 43 | 968 | 97.2 | 194 | 5 | ABB76827 Mutant Hu |
| 44 | 966 | 97.0 | 194 | 3 | AAB13719 H. insole |
| 45 | 966 | 97.0 | 194 | 6 | Aae34659 Humicola |

RESULT 1

AAR95051
ID AAR95051 standard; protein; 246 AA.
XX AC AAR95051;
XX DT 17-DEC-1996 (first entry)
XX DE H. insolens lipase.
XX KW lipase; detergent; dishwashing; laundry; short-chain lipid.
XX OS Humicola insolens.
XX FH Key Location/Qualifiers
FT Peptide 1..35
FT Protein /label= signal_peptide
FT FT 36..246
FT FT /label= mature_protein
XX PN WO9613580-A1.
XX PD 09-MAY-1996.
XX PF 26-OCT-1995; 95WO-DK000427.
XX PR 26-OCT-1994; 94DK-00001240.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Sandal T, Kauppinen S, Kofod LV;
XX DR WPI; 1996-239493/24.
XX DR N-PSDB; AAT29401.
XX PS Isolated DNA encoding lipolytic enzyme - derived from Humicola insolens
XX PT DSM1800, used partic. as detergent additive for laundry and dishwashing
XX PT compsns.
XX PT Disclosure; Page 52; 63pp; English.

need more seq claim 45

ALIGNMENTS

The present sequence is that of an enzyme with lipolytic activity, derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of about 20-21 kDa, a pI in the range of 703, a pH optimum of about 8 and has specificity towards short-chain lipid substrates. It can be used as a detergent additive, partic. in compsns. for laundry washing or dishwashing

XX SQ Sequence 246 AA;
 Query Match 100.0%; Score 996; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2.9e-98;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLGAIENGLSSGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
 DB 36 QLGAIENGLSSGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 95
 QY 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVWAGYSOGAALIAAIVSELG 120
 DB 96 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVWAGYSOGAALIAAIVSELG 155
 QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLITPAHLSYITIEA 180
 DB 156 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLITPAHLSYITIEA 215
 QY 181 RGEAARFLDRIRA 194
 DB 216 RGEAARFLDRIRA 229

RESULT 2
 AAM48435
 ID AAM48435 standard; protein; 194 AA.
 XX AC AAM48435;
 XX DT 29-AUG-2003 (revised)
 DT 25-JUN-2002 (first entry)
 XX DE Wild-type Humicola insolens mature cutinase.
 XX KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin.
 XX OS Humicola insolens; strain DSM 1800.
 XX PN WC200192502-A1.
 XX PD 06-DEC-2001.
 XX PF 22-MAY-2001; 2001WO-DK000350.
 XX PR 02-JUN-2000; 2000DK-00000861.
 PR 23-OCT-2000; 2000DK-00001577.
 PR 24-NOV-2000; 2000DK-00001772.
 PR 19-JAN-2001; 2001DK-00000100.
 XX PA (NOVO) NOVOZYMES AS.
 XX SV Svendsen A, Glad SOS, Fukuyama S, Matsui T;
 XX WPI; 2002-216714/27.
 XX PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 PT oligomers of poly(ethylene terephthalate), comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens
 PT cutinase.
 XX PS Disclosure; Page 36; 41pp; English.
 XX CC The present sequence is the wild-type mature cutinase from Humicola
 CC insolens strain DSM 1800, which was used to generate mutant cutinases
 CC (see ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes
 CC capable of hydrolysing the substrate cutin. The mutant cutinases have
 CC improved thermostability, and are used for enzymatic hydrolysis of cyclic
 CC oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn
 CC or fabric from poly(ethylene terephthalate) fibers. (Updated on 29-AUG-
 CC 2003 to standardise OS field)
 XX SQ Sequence 194 AA;

Query Match 99.5%; Score 991; DB 5; Length 194;
 Best Local Similarity 99.5%; Pred. No. 7.1e-98;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLGAIENGLSSGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
 DB 1 QLGAIENGLSSGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
 QY 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVWAGYSOGAALIAAIVSELG 120
 DB 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVWAGYSOGAALIAAIVSELG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLITPAHLSYITIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLITPAHLSYITIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194

RESULT 3
 AAE34646
 ID AAE34646 standard; protein; 194 AA.
 XX AC AAE34646;
 XX DT 14-MAY-2003 (first entry)
 XX DE Humicola insolens cutinase protein.
 XX KW Lipolytic enzyme; cutinase; lipase; paper; enzyme.
 XX OS Humicola insolens.
 XX PN WO200295127-A2.
 XX PD 28-NOV-2002.
 XX PF 17-MAY-2002; 2002WO-DK000326.
 XX PR 21-MAY-2001; 2001DK-00000813.
 XX PA (NOVO) NOVOZYMES AS.
 XX PI Borch K, Lund H, Sharyo M, Sakaguchi H, Pedersen HH;
 PI Fitzhenry JW;
 XX WPI; 2003-156764/15.
 XX PT Making paper comprises preparing pulp from recycled paper, and treating
 PT pulp with a lipolytic enzyme, which is able to hydrolyze a polymer
 PT comprising a vinyl acetate monomer.
 XX PS Disclosure; Page 36-37; 40pp; English.
 XX CC The invention relates to the use of certain lipolytic enzymes such as
 CC cutinases and lipases in the manufacture of paper and paper products from
 CC recycled paper. The invention also relates to a method of making paper
 CC which involves preparing a pulp recycled paper, treating the pulp with a
 CC lipolytic enzyme which is able to hydrolyse a polymer comprising vinyl
 CC acetate monomer and making paper from the treated pulp. The method is
 CC used for making paper from recycled paper. The method of the invention
 CC provides stickies control and/or de-inking. The present sequence is
 CC Humicola insolens cutinase protein
 XX SQ Sequence 194 AA;

Query Match 99.5%; Score 991; DB 6; Length 194;
 Best Local Similarity 99.5%; Pred. No. 7.1e-98;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLGAIENGLSSGANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVG 60
 Db 1 QLGAIENGLSSGANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVG 60
 QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVVGAGYSQGAALIAAAVSELG 120
 Db 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVVGAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 Db 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 Db 181 RGEAARFLDRIRA 194
 RESULT 4
 AAB13715
 ID AAB13715 standard; protein; 194 AA.
 XX AC AAB13715;
 XX DT 17-NOV-2000 (first entry)
 XX DE H. insolens mutant cutinase, E179Q substitution.
 XX KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX OS Humicola insolens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 179 /note= "Wild-type Glu substituted by Gln"
 XX PN WO200034450-A1.
 XX PD 15-JUN-2000.
 XX PF 03-DEC-1999; 99WO-DK000678.
 XX PR 04-DEC-1998; 98DK-00001604.
 PR 09-DEC-1998; 98US-0111591P.
 PR 09-MAR-1999; 99DK-00000330.
 PR 16-MAR-1999; 99US-0124671P.
 XX PA (NOVO) NOVO-NORDISK AS.
 PI Abo M, Fukuyama S, Svendsen A, Matsui T;
 XX WPI; 2000-482424/42.
 XX Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid.
 XX Example 1; Page; 79pp; English.
 XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
 CC cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
 CC thermostability are useful since they can withstand higher processing
 CC temperatures. Note: the present sequence is not shown in the
 CC specification but is derived from the H. insolens wild-type cutinase
 CC sequence given in SEQ ID 2 of patent: US 5,827,719

SQ Sequence 194 AA;
 Query Match 99.2%; Score 988; DB 3; Length 194;
 Best Local Similarity 99.0%; Pred. No. 1.5e-97;
 Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAIENGLSSGANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVG 60
 Db 1 QLGAIENGLSSGANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVG 60
 QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVVGAGYSQGAALIAAAVSELG 120
 Db 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVVGAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 Db 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 Db 181 RGEAARFLDRIRA 194
 RESULT 5
 AAB13706
 ID AAB13706 standard; protein; 194 AA.
 XX AC AAB13706;
 XX DT 17-NOV-2000 (first entry)
 XX DE H. insolens mutant cutinase, E47K substitution.
 XX KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX OS Humicola insolens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 47 /note= "Wild-type Glu substituted by Lys"
 XX PN WO200034450-A1.
 XX PD 15-JUN-2000.
 XX PF 03-DEC-1999; 99WO-DK000678.
 XX PR 04-DEC-1998; 98DK-00001604.
 PR 09-DEC-1998; 98US-0111591P.
 PR 09-MAR-1999; 99DK-00000330.
 PR 16-MAR-1999; 99US-0124671P.
 XX PA (NOVO) NOVO-NORDISK AS.
 PI Abo M, Fukuyama S, Svendsen A, Matsui T;
 XX WPI; 2000-482424/42.
 XX Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid.
 XX Claim 16; Page; 79pp; English.
 XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
 CC cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from

PS Claim 8; Page; 4lpp; English.

XX The present invention relates to wild-type mature cutinase from Humicola

CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant

CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic

CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases

CC have improved thermostability, and are used for enzymatic hydrolysis of

CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing

CC of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the

CC present sequence in not shown in the specification, but is derived from

CC the wild-type cutinase sequence shown on page 36

XX Sequence 194 AA;

SQ

Query Match 99.1%; Score 987; DB 5; Length 194;

Best Local Similarity 99.0%; Pred. No. 1.9e-97;

Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIOGVGG 60

DB 1 QLGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIOGVGG 60

QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

DB 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

QY 181 RGEAARFLDRIRA 194

DB 181 RGEAARFLDRIRA 194

RESULT 8

ABB76838

ID ABB76838 standard; protein; 194 AA.

XX AC ABB76838;

XX

DT 25-JUN-2002 (first entry)

DE

DE Mutant Humicola insolens mature cutinase #12.

XX

XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.

XX

OS Humicola insolens; strain DSM 1800.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT Misc-difference 174

FT /note= "Wild-type Leu substituted by Phe"

XX

XX WO200192502-A1.

XX

PD 06-DEC-2001.

XX

XX 22-MAY-2001; 2001WO-DK000350.

XX

XX 02-JUN-2000; 2000DK-00000861.

PR 23-OCT-2000; 2000DK-00001577.

PR 24-NOV-2000; 2000DK-00001772.

PR 19-JAN-2001; 2001DK-00000100.

XX

XX (NOVO) NOVOZYMES AS.

XX

XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;

XX

DR WPI; 2002-216714/27.

XX

XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic

PT oligomers of poly(ethylene terephthalate), comprises a substitution of

PT amino acid residues corresponding to positions of Humicola insolens

PT cutinase.

XX Claim 8; Page; 4lpp; English.

XX The present invention relates to wild-type mature cutinase from Humicola

CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant

CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic

CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases

CC have improved thermostability, and are used for enzymatic hydrolysis of

CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing

CC of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the

CC present sequence in not shown in the specification, but is derived from

CC the wild-type cutinase sequence shown on page 36

XX Sequence 194 AA;

SQ

Query Match 99.1%; Score 987; DB 5; Length 194;

Best Local Similarity 99.0%; Pred. No. 1.9e-97;

Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIOGVGG 60

DB 1 QLGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIOGVGG 60

QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

DB 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

QY 181 RGEAARFLDRIRA 194

DB 181 RGEAARFLDRIRA 194

RESULT 9

AAE34652

ID AAE34652 standard; protein; 194 AA.

XX AC AAE34652;

XX

DT 14-MAY-2003 (first entry)

XX

XX Humicola insolens cutinase mutant protein #4.

DE

XX Lipolytic enzyme; cutinase; lipase; paper; enzyme; mutant; mutein.

XX

XX Humicola insolens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT Misc-difference 47

FT /note= "Wild-type Glu substituted with Lys"

XX

XX WO200295127-A2.

XX

XX 28-NOV-2002.

XX

XX 17-MAY-2002; 2002WO-DK000326.

XX

XX 21-MAY-2001; 2001DK-00000813.

XX

XX (NOVO) NOVOZYMES AS.

XX

XX Borch K, Lund H, Sharyo M, Sakaguchi H, Pedersen HH;

PI Fitzhenry JW;

XX

XX WPI; 2003-156764/15.

XX

XX Making paper comprises preparing pulp from recycled paper, and treating

PT pulp with a lipolytic enzyme, which is able to hydrolyze a polymer
 XX comprising a vinyl acetate monomer.
 PS Disclosure; Page; 40pp; English.
 XX
 CC The invention relates to the use of certain lipolytic enzymes such as
 CC cutinases and lipases in the manufacture of paper and paper products from
 CC recycled paper. The invention also relates to a method of making paper
 CC which involves preparing a pulp recycled paper, treating the pulp with a
 CC lipolytic enzyme which is able to hydrolyse a polymer comprising vinyl
 CC acetate monomer and making paper from the treated pulp. The method is
 CC used for making paper from recycled paper. The method of the invention
 CC provides stickies control and/or de-inking. The present sequence is
 CC Humicola insolens cutinase mutant protein (B47K). Note: This sequence is
 CC not shown in the specification but is derived from Humicola insolens
 CC cutinase protein shown as SEQ ID NO: 1 in pages 36-37 of the
 CC specification (AAE34646)
 XX
 XX Sequence 194 AA;
 SQ
 Query Match 99.1%; Score 987; DB 6; Length 194;
 Best Local Similarity 99.0%; Pred. No. 1.9e-97;
 Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNGITVGPALANGLESHERNIWIQVGG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNGITVGPALANGLESHERNIWIQVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRETKVFCNVGDAVCTGTLITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRETKVFCNVGDAVCTGTLITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 10
 AAB13707
 ID AAB13707 standard; protein; 194 AA.
 XX
 AC AAB13707;
 XX
 XX 17-NOV-2000 (first entry)
 DT
 DE H. insolens mutant cutinase, E179X substitution.
 XX
 KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX
 XX Humicola insolens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 179
 FT /note= "Wild-type Glu substituted by Asn or Gln"
 FT
 XX WO200034450-A1.
 PN
 XX 15-JUN-2000.
 PD
 XX 03-DEC-1999; 99WO-DK000678.
 PP
 XX 04-DEC-1998; 98DK-00001604.
 PR 09-DEC-1998; 98US-0111591P.
 PR 09-MAR-1999; 98DK-00000330.
 PR 16-MAR-1999; 99US-0124671P.
 PR

PA (NOVO) NOVO-NORDISK AS.
 XX Abo M, Fukuyama S, Svendsen A, Matsui T;
 PI WPI; 2000-482424/42.
 XX
 XX Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid.
 XX
 XX Claim 16; Page; 79pp; English.
 PS
 CC Site-directed mutagenesis was carried out on wild-type Humicola insolens
 CC cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysis of the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
 CC thermostability are useful since they can withstand higher processing
 CC temperatures. Note: the present sequence is not shown in the
 CC specification but is derived from the H. insolens wild-type cutinase
 CC sequence given in SEQ ID 2 of patent: US 5,827,719
 XX
 XX Sequence 194 AA;
 SQ
 Query Match 98.9%; Score 985; DB 3; Length 194;
 Best Local Similarity 99.0%; Pred. No. 3.2e-97;
 Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNGITVGPALANGLESHERNIWIQVGG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNGITVGPALANGLESHERNIWIQVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRETKVFCNVGDAVCTGTLITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRETKVFCNVGDAVCTGTLITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 11
 ABB76839
 ID ABB76839 standard; protein; 194 AA.
 XX
 AC ABB76839;
 XX
 XX 25-JUN-2002 (first entry)
 DT
 XX Mutant Humicola insolens mature cutinase #13.
 DE
 XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
 KW Humicola insolens; strain DSM 1800.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 49
 FT /note= "Wild-type His substituted by Tyr"
 FT
 XX WO200192502-A1.
 PN
 XX 06-DEC-2001.
 PD
 XX 22-MAY-2001; 2001WO-DK000350.
 PF
 XX 02-JUN-2000; 2000DK-00000861.
 PR

FT XX /note= "wild-type Arg substituted by Pro"

PN XX WO200034450-A1.

XX XX 15-JUN-2000.

PF 03-DEC-1999; 99WO-DK000678.

XX 04-DEC-1998; 98DK-00001604.

PR 09-DEC-1998; 98US-0111591P.

PR 09-MAR-1999; 99DK-00000330.

PR 16-MAR-1999; 99US-0124671P.

XX (NOVO) NOVO-NORDISK AS.

XX Abo M, Fukuyama S, Svendsen A, Matsui T;

PI WPI; 2000-482424/42.

XX Thermostable variant of parent fungal cutinase useful for dyeing

PT polyester yarn or fabric, comprises substitution of amino acid residues

PT at predetermined positions from the N-terminal amino acid.

XX Claim 16; Page; 79pp; English.

XX Site-directed mutagenesis was carried out on wild-type Humicola insolens

CC cutinase, to produce the present sequence. The introduced substitution

CC improves the thermostability of the cutinase enzyme. Cutinases are

CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase

CC may be used in the enzymatic hydrolysis of cyclic oligomers of

CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from

CC poly(ethylene terephthalate) fibers. Cutinase variants with improved

CC thermostability are useful since they can withstand higher processing

CC temperatures. Note: the present sequence is not shown in the

CC specification but is derived from the H. insolens wild-type cutinase

CC sequence given in SEQ ID 2 of patent: US 5,827,719

XX Sequence 194 AA;

SQ Query Match 98.8%; Score 984; DB 3; Length 194;

Best Local Similarity 99.0%; Pred. No. 4e-97;

Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHPNIWIQVGG 60

Db 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHPNIWIQVGG 60

Qy 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAAVSELG 120

Db 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAAVSELG 120

Qy 121 AVKEQKGVALLFGYTQNLQNRGGIANYPRRTKVFNCNVDGAVCTGTLLITPAHLSYTIEA 180

Db 121 AVKEQKGVALLFGYTQNLQNRGGIANYPRRTKVFNCNVDGAVCTGTLLITPAHLSYTIEA 180

Qy 181 RGEAARFLDRIRA 194

Db 181 RGEAARFLDRIRA 194

RESULT 14

AAE34649

ID AAE34649 standard; protein; 194 AA.

XX AAE34649;

XX 14-MAY-2003 (first entry)

XX Humicola insolens cutinase mutant protein #1.

DE Lipolytic enzyme; cutinase; lipase; paper; enzyme; mutant; mutein.

KW Humicola insolens.

XX OS

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 51

FT /note= "Wild-type Arg substituted with Pro"

XX WO200295127-A2.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-DK000326.

XX 21-MAY-2001; 2001DK-00000813.

XX (NOVO) NOVOZYMES AS.

XX Borch K, Lund H, Sharyo M, Sakaguchi H, Pedersen HH;

PI Fitzhenry JW;

XX WPI; 2003-156764/15.

DR Making paper comprises preparing pulp from recycled paper, and treating

XX pulp with a lipolytic enzyme, which is able to hydrolyze a polymer

PT comprising a vinyl acetate monomer.

PT Disclosure; Page; 40pp; English.

XX The invention relates to the use of certain lipolytic enzymes such as

CC cutinases and lipases in the manufacture of paper and paper products from

CC recycled paper. The invention also relates to a method of making paper

CC which involves preparing a pulp recycled paper, treating the pulp with a

CC lipolytic enzyme which is able to hydrolyse a polymer comprising vinyl

CC acetate monomer and making paper from the treated pulp. The method is

CC used for making paper from recycled paper. The method of the invention

CC provides stickies control and/or de-inking. The present sequence is

CC Humicola insolens cutinase mutant protein (R51P). Note: This sequence is

CC not shown in the specification but is derived from Humicola insolens

CC cutinase protein shown as SEQ ID NO: 1 in pages 36-37 of the

CC specification (AAE34646)

XX Sequence 194 AA;

SQ Query Match 98.8%; Score 984; DB 6; Length 194;

Best Local Similarity 99.0%; Pred. No. 4e-97;

Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHPNIWIQVGG 60

Db 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHPNIWIQVGG 60

Qy 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAAVSELG 120

Db 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAAVSELG 120

Qy 121 AVKEQKGVALLFGYTQNLQNRGGIANYPRRTKVFNCNVDGAVCTGTLLITPAHLSYTIEA 180

Db 121 AVKEQKGVALLFGYTQNLQNRGGIANYPRRTKVFNCNVDGAVCTGTLLITPAHLSYTIEA 180

Qy 181 RGEAARFLDRIRA 194

Db 181 RGEAARFLDRIRA 194

RESULT 15

AAE34649

ID AAE34649 standard; protein; 194 AA.

XX AAE34649;

XX 17-NOV-2000 (first entry)

XX H. insolens mutant cutinase, E6X/L138I substitution.

XX OS

KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
KW protein co-ordinate.
XX
OS Humicola insolens.
OS Synthetic.
XX

XX Key Location/Qualifiers
FH Misc-difference 6 /note= "Wild-type Glu substituted by Asn or Gln"
FT
FT Misc-difference 138
FT /note= "Wild-type Leu substituted by Ile"
XX

FN W0200034450-A1.
XX
XX 15-JUN-2000.
XX
XX 03-DEC-1999; 99WO-DK000678.
XX
XX 04-DEC-1998; 98DK-00001604.
PR 09-DEC-1998; 98US-0111591P.
PR 09-MAR-1999; 99DK-00000330.
PR 16-MAR-1999; 99US-0124671P.
XX
XX (NOVO) NOVO-NORDISK AS.
PA

XX Abo M, Fukuyama S, Svendsen A, Matsui T;
PI WPI; 2000-482424/42.
XX
XX Thermostable variant of parent fungal cutinase useful for dyeing
PT polyester yarn or fabric, comprises substitution of amino acid residues
PT at predetermined positions from the N-terminal amino acid.
XX
XX Claim 16; Page; 79pp; English.

XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
CC cutinase, to produce the present sequence. The introduced substitution
CC improves the thermostability of the cutinase enzyme. Cutinases are
CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
CC may be used in the enzymatic hydrolysis of cyclic oligomers of
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
CC thermostability are useful since they can withstand higher processing
CC temperatures. Note: the present sequence is not shown in the
CC specification but is derived from the H. insolens wild-type cutinase
CC sequence given in SEQ ID 2 of patent: US 5,827,719
XX

SQ Sequence 194 AA;
Query Match 98.7%; Score 983; DB 3; Length 194;
Best Local Similarity 98.5%; Pred. No. 5.2e-97;
Matches 191; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGESHIRNIWIOGVGG 60
DB 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGESHIRNIWIOGVGG 60
OY 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVGYSQGAALIAAAVSELG 120
DB 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVGYSQGAALIAAAVSELG 120
OY 121 AVKEQVKGVALFGYTNLONRGIANYPRTKVFNCVGDVCTGLTIITPAHLSYTIEA 180
DB 121 AVKEQVKGVALFGYTNLONRGIANYPRTKVFNCVGDVCTGLTIITPAHLSYTIEA 180
OY 181 RGEARFLDRIRA 194
DB 181 RGEARFLDRIRA 194

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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:52:09 ; Search time 43 Seconds
(without alignments)
434.094 Million cell updates/sec

Title: us-08-817-997-2_copy_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPD.....SYTIEARGEAEARFLDRIRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 593.5 | 59.6 | 228 | 1 S20448 | cutinase (EC 3.1.-) |
| 2 | 576 | 57.8 | 224 | 1 B27451 | cutinase (EC 3.1.-) |
| 3 | 564 | 56.6 | 223 | 1 S21427 | cutinase - fungus |
| 4 | 550.5 | 55.3 | 228 | 1 A27451 | cutinase (EC 3.1.-) |
| 5 | 545 | 54.7 | 230 | 1 UVFUS | cutinase (EC 3.1.-) |
| 6 | 189.5 | 19.0 | 217 | 2 F70756 | probable cutinase |
| 7 | 188.5 | 18.9 | 219 | 2 A70734 | probable cutinase |
| 8 | 178 | 17.9 | 226 | 2 A70565 | probable cutinase |
| 9 | 167.5 | 16.8 | 247 | 2 H70364 | probable cutinase |
| 10 | 115.5 | 11.6 | 187 | 2 F70796 | probable cutinase |
| 11 | 98 | 9.8 | 174 | 2 G70987 | probable cutinase |
| 12 | 96 | 9.6 | 336 | 2 F70887 | hypothetical prote |
| 13 | 89.5 | 9.0 | 420 | 2 T35575 | hypothetical prote |
| 14 | 88 | 8.8 | 1293 | 2 B85557 | enterobactin synth |
| 15 | 88 | 8.8 | 1293 | 2 A90707 | enterobactin synth |
| 16 | 88 | 8.8 | 1356 | 2 T18521 | beta transducin-l1 |
| 17 | 88 | 8.8 | 3355 | 2 E83641 | probable hemagglut |
| 18 | 87 | 8.7 | 336 | 2 C86921 | conserved hypothet |
| 19 | 87 | 8.7 | 892 | 2 S76350 | hypothetical prote |
| 20 | 86.5 | 8.7 | 123 | 2 B86566 | hypothetical prote |
| 21 | 86 | 8.6 | 357 | 2 A95190 | hypothetical prote |
| 22 | 86 | 8.6 | 357 | 2 B98056 | hypothetical prote |
| 23 | 86 | 8.6 | 5627 | 2 C83339 | hypothetical prote |
| 24 | 85.5 | 8.6 | 302 | 2 S71334 | acetyl xylan ester |
| 25 | 85.5 | 8.6 | 382 | 2 A87548 | 3-carboxy-cis,cis- |
| 26 | 85.5 | 8.6 | 6486 | 2 T31076 | tyrocidine synthet |
| 27 | 84.5 | 8.5 | 2082 | 2 T37056 | probable multi-dom |
| 28 | 84.5 | 8.5 | 4848 | 2 T30289 | pristinamycin I sy |
| 29 | 83.5 | 8.4 | 338 | 2 A83946 | stage V sporulatio |

30 83.5 8.4 665 2 F97032 beta-glucosidase f
31 83 8.3 329 2 B46678 endoglycosidase F3
32 82.5 8.3 398 2 D83214 conserved hypothet
33 82 8.2 619 2 H84416 hypothetical prote
34 81.5 8.2 317 2 B82637 bifunctional bioti
35 81.5 8.2 453 2 H81308 Glu-trNAGln amidot
36 81 8.1 202 2 D71005 hypothetical prote
37 81 8.1 380 2 B70544 probable histidino
38 81 8.1 592 1 S13391 endo-1,4-beta-xyla
39 80.5 8.1 506 2 B72396 sugar kinase, FGGY
40 79.5 8.0 200 2 A69903 hypothetical prote
41 79.5 8.0 342 2 A97184 stage V sporulatio
42 79.5 8.0 749 2 E95889 probable dehydroge
43 79.5 8.0 1075 2 T48805 hypothetical prote
44 79 7.9 322 2 AH3011 thioresoxin trxA l
45 79 7.9 331 2 G98272 probable thioresox

ALIGNMENTS

RESULT 1

S20448

cutinase (EC 3.1.-) - rice blast fungus

C:Species: Magnaporthe grisea (rice blast fungus)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S20448

R:Seigward, J.A.; Chumley, F.G.; Valent, B.

Mol. Gen. Genet. 232, 174-182, 1992

A:Title: Cloning and analysis of CUT1, a cutinase gene from Magnaporthe grisea.

A:Reference number: S20448; MUID:92212279; PMID:1557023

A:Accession: S20448

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-228 <SWE>

A:Cross-references: UNIPROT:P30272; UNIPARC:UPI000012871C; GB:X61500; NID:G2928; PIDN:CA

C:Genetics:

A:Gene: CUT1

C:Superfamily: cutinase

C:Keywords: hydrolase

Query Match

Best Local Similarity 59.6%; Score 593.5; DB 1; Length 228;

Matches 116; Conservative 27; Mismatches 51; Indels 1; Gaps 1;

Qy 1 QLGAIENGLESGSANACPDAILIPARGSTEPQNGITVGPALANGLESIRN-INTQGVG 59

Db 33 QLSNVRNDLISGNAACPSVILIIFARASGEVGNMGLSAGTNVASRLERFRNDIWWQGVG 92

Qy 60 GPYDAALATNPLPRGTSQANIDEGKRLFPALANQKCPNTFVWAGYSQGAALIAAAVSELS 119

Db 93 DPYDAALSPNPLPAGTTQGAIDEAKMFTLANTKCPNAAVWAGYSQGTAVMFNAVSEMP 152

Qy 120 GAVKEQKGVVALFGYTONLQNRGIANVPRRTKVFQCVGDAVCTGTLLITPAHLSYTTRE 179

Db 153 AAVQDQIKGVVLFVGTKNLQNRGIRIPDPPTKTEVYCNASDAVCFGLTFLPAHFLYTTRE 212

Qy 180 ARGEAARFLDRIRA 194

Db 213 SSIAAPNWLIRQIRA 227

RESULT 2

B27451

cutinase (EC 3.1.-) precursor - anthracnose fungus (Colletotrichum gloeosporioides) (f

C:Species: Glomerella cingulata, Colletotrichum gloeosporioides

C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C:Accession: B27451

R:Ettinger, W.F.; Thukral, S.K.; Kolattukudy, P.E.

Biochemistry 26, 7883-7892, 1987

A:Title: Structure of cutinase gene, cDNA, and the derived amino acid sequence from phyt

A:Reference number: A90524

A:Accession: B27451

```
A:Molecule type: DNA
A:Residues: 1-224 <ETT>
A:Cross-references: UNIPROT:P11373; UNIPARC:UPI000012871A
C:Comment: The cleavage site for the signal peptide is unknown.
C:Genetics:
A:Introns: 63/3
C:Superfamily: cutinase
C:Keywords: hydrolase
F:46-194,125-187/Disulfide bonds: #status predicted
F:96,136,204/Active site: Asp, Ser, His #status predicted

Query Match 57.8%; Score 576; DB 2; Length 224;
Best Local Similarity 58.5%; Pred. No. 1.5e-44;
Matches 110; Conservative 28; Mismatches 48; Indels 2; Gaps 1;

QY 7 NGLSGSANACPDAILIFARGSTPGNMGITVGPALANGLESH--HIRNIWIOGVGGPYDA 64
Db 36 NELETGSSSNACPKVIYIFARASTEPGNMGISAGPIVADALERIYANNVWVQGVGGPYLA 95

QY 65 ALATNPLPGTSGQANTDEGKRLFALANOKCPNTPVAVGGYSQGAALIAAAVSELGAVKE 124
Db 96 DLASNPLPGTSSAALNEARLFTLANTKCPNAAIVSGGYSQGTAVWAGSISGLSTIKN 155

QY 125 QVKGVALFGYTONLQNRGGIANYPRERTKVCNVGDVAVCTGLTIITPAHLSYTIARGE 184
Db 156 QIKGVVLFYGTNQLNQLGRIPNPFSTKTEYVCALADAVCYGTLFILPAHFLYQADAATS 218

QY 185 ARFLRDRI 192
Db 216 PRFLQARI 223

RESULT 3
S21427
cutinase - fungus (Ascochyta rabiei)
C:Species: Ascochyta rabiei
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S21427
R:Tenhaken, R.; Barz, W.
submitted to the EMBL Data Library, April 1992
A:Description: Characterization and cloning of cutinase from Ascochyta rabiei.
A:Reference number: S21427
A:Accession: S21427
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-223 <TEN>
A:Cross-references: UNIPROT:P29292; UNIPARC:UPI0000128716; EMBL:X65628; NID:g2472; PIDN:
C:Genetics:
A:Introns: 63/3
C:Superfamily: cutinase

Query Match 56.6%; Score 564; DB 1; Length 223;
Best Local Similarity 58.8%; Pred. No. 1.8e-43;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESH--IRNIWIOGVGGPYD 63
Db 34 ISELEQSSSSCPKAILIFARGSTIENGWGVGAGFAVASALRAYGADQIIVWGVGGPYT 93

QY 64 ALATNPLPGTSGQANTDEGKRLFALANOKCPNTPVAVGGYSQGAALIAAAVSELGAVK 123
Db 94 ADLPSNPLPGTSSQASINEAVRLFNEANTKCPSTPIVAGGYSQGTAVWAGAIKPLD-AVR 152

QY 124 EQKGVVALFGYTONLQNRGGIANYPRERTKVCNVGDVAVCTGLTIITPAHLSYTIARGE 183
Db 153 ARVVGTVLFGYTONQNNKGIKDYQPDQLQVYCEVDLVCDGTLTIITVSHFLYLEAAGP 212

QY 184 ARFLRDRI 194
Db 213 APEFLSKIGA 223

RESULT 4
```

```
A27451
cutinase (EC 3.1.1.-) precursor - anthractnose fungus (Colletotrichum capsici) (fragments
C:Species: Colletotrichum capsici
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27451
R:Ettinger, W.F.; Thukral, S.K.; Kolattukudy, P.E.
Biochemistry 26, 7883-7892, 1987
A:Title: Structure of cutinase gene, cDNA, and the derived amino acid sequence from phyto
A:Reference number: A90524
A:Accession: A27451
A:Molecule type: DNA
A:Residues: 1-228 <ETT>
A:Cross-references: UNIPROT:P10951; UNIPARC:UPI0000128719
C:Comment: The cleavage site for the signal sequence is not known.
C:Genetics:
A:Introns: 66/3
C:Superfamily: cutinase
C:Keywords: hydrolase
F:49-198,129-191/Disulfide bonds: #status predicted
F:99,140,208/Active site: Asp, Ser, His #status predicted

Query Match 55.3%; Score 550.5; DB 2; Length 228;
Best Local Similarity 57.1%; Pred. No. 3e-42;
Matches 108; Conservative 27; Mismatches 51; Indels 3; Gaps 2;

QY 7 NGLSGSANACPDAILIFARGSTPGNMGITVGPALANGLESH--IRNIWIOGVGGPYDA 64
Db 39 NELESGSSSNCPKVIYIFARASTEPGNMGISAGPIVADALESRYGASQVWVQGVGGPYSA 98

QY 65 ALATNF-LPRGTQANTDEGKRLFALANOKCPNTPVAVGGYSQGAALIAAAVSELGAVK 123
Db 99 DLASNPLPGTSGKVAINEAKRLFTLANTKCPNAAIVAGGYSQGTAVWAGSISGLSTIQ 158

QY 124 EQKGVVALFGYTONLQNRGGIANYPRERTKVCNVGDVAVCTGLTIITPAHLSYTIARGE 183
Db 159 NQIKGVVLSAITKMLNQLGRIPNPFSTKTEYVCALADAVCYGTLFILPAHFLYQADAATS 218

QY 184 ARFLRDRI 192
Db 219 APRFLAARI 227

RESULT 5
UVFUS
cutinase (EC 3.1.1.-) precursor - fungus (Fusarium solani)
C:Species: Fusarium solani f.sp. pisi
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A32836; A00731; E00731; A61421
R:Soliday, C.L.; Dickman, M.B.; Kolattukudy, P.E.
J. Bacteriol. 171, 1942-1951, 1989
A:Title: Structure of the cutinase gene and detection of promoter activity in the 5'-fla
A:Reference number: A32836; MUID:8919761; PMID:2703464
A:Accession: A32836
A:Molecule type: DNA
A:Residues: 1-47, 'A', 49-93, 'A', 95-230 <SOL>
A:Cross-references: UNIPROT:P00590; UNIPARC:UPI00001688FB; GB:M29759; NID:g168147; PIDN:
A:Note: the authors translated the codon GCA for residue 94 as Arg
R:Soliday, C.L.; Flurkey, W.H.; Okita, T.W.; Kolattukudy, P.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 3939-3943, 1984
A:Title: Cloning and structure determination of cDNA for cutinase, an enzyme involved in
A:Reference number: A00731
A:Accession: A00731
A:Molecule type: mRNA
A:Residues: 1-230 <S02>
A:Cross-references: UNIPARC:UPI0000128702; GB:K02640; NID:g168145; PIDN:AAA33334.1; PID:
A:Accession: B00731
A:Molecule type: protein
A:Residues: 57-94,113-142,183-192 <S03>
A:Cross-references: UNIPARC:UPI0000172739; UNIPARC:UPI000017273A; UNIPARC:UPI000017273B
R:Soliday, C.L.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 114, 1017-1022, 1983
A:Title: Primary structure of the active site region of fungal cutinase, an enzyme invol
A:Reference number: A61421; MUID:83308716; PMID:6412706
```

A:Accession: A61421
A:Molecule type: protein
A:Residues: 113-142 <SQ4>
A:CROSS-references: UNIPARC:UPI000017273A
R:Lin, T.S.; Kolattukudy, P.E.
Eur. J. Biochem. 106, 341-351, 1980

A>Title: Structural studies on cutinase, a glycoprotein containing novel amino acids and
A:Reference number: A44665; MUID:90245930; PMID:7398618
A:Contents: annotation; identification of glucuronylated amino end
C:Comment: This enzyme catalyzes the hydrolysis of cutin, a polyester that forms the str
C:Comment: Southern blot results suggest that the genome contains two copies of the cuti
C:Genetics: 64/3
A:introns:
C:Superfamily: cutinase
C:Keywords: blocked amino end; glycoprotein; hydrolase
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-230/Product: cutinase #status predicted <MAT>
F:32/Modified site: glucuronylated amino end (Gly) (in mature form) #status experimental
F:125-187/Disulfide bonds: #status experimental
F:136,204/Active site: Ser, His #status experimental

Query Match 54.7%; Score 545; DB 1; Length 230;
Best Local Similarity 54.8%; Pred. No. 9.5e-42;
Matches 108; Conservative 32; Mismatches 53; Indels 4; Gaps 3;

Qy 1 QLG-AIENGLESANACPDAILIFARGSTPEPGNGITVGPALANGLESHI--RNIIQG 57
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 30 QLGRITRDDLLINGNSASCRDVIYFARGSTETNGLG-TLGPSIASNLSEAFKCGVWVG 88
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Qy 58 VGGPVDAALATNP LPRGTQANTIDEGKRFLPALANKPCNTPEVVAGGYSGQAALIAAVSE 117
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 89 VGGAYRVATLGDNALPRTGSAAIREMLGLFOQAKTKCPDATLIAGGYSGQAALAASAIST 148
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Qy 118 LSGAVKEQVKVALFCVTQNLRGGTIANYPRETKVPNCNVDAVCCTCLITPAHLSVT 177
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 149 LSARNDKIAGTVLFGTKNLQRGRIPNYPADRTKVFCTNGLVCTSLVAAPHLAYG 208
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Qy 178 IEARGEAEARFLDRIRA 194
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 209 PDARGAPEFLIEKVRA 225
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 6
F70756
probable cutinase precursor with N-terminal signal sequence - Mycobacterium tuberculosis
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70756
R:Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998
A:Authors: Squares, K.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70756
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-217 <COL>
A:CROSS-references: UNIPROT:Q10837; UNIPARC:UPI000003181B; GB:Z74025; GB:AL123456; NID:9
A:A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv1984c
C:Superfamily: cutinase

Query Match 19.0%; Score 189.5; DB 2; Length 217;
Best Local Similarity 30.8%; Pred. No. 1e-09;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

Qy 8 GLEESANACPDAILIFARGSTPEPGNGITVGPALANGLESHIRNIIVGVGPPYDALA 67
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 26 GGAAHADPCSIAIVFAFGTHQASGLIG-DVGEAFVDLSLTQS-----VGGRSIGYYA 76
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

[illegible]

E70796

Probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: E70796
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70796
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-187 <COL>
A;Cross-references: UNIPARC:UPI000016537B; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CA
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV3724
C;Superfamily: cutinase

| | Query Match | 11.6% | Score 115.5; | DB 2; | Length 187; |
|----------------------|-------------|-------------------|--------------|------------|-------------|
| Bst Local Similarity | 27.6%; | Pred. No. 0.0039; | | | |
| Matches | 45; | Conservative | 22; | Mismatches | 73; |
| Gaps | Indels | 23; | Gaps | 7; | |

Qy 51 RNWITQGCGPYDAALATNFLPRGTSQAANI DEGRKLFALANOKCPNTFVAGYSQGAAL 110
::: | ::| :
Db 27 KSLGVYAVNPASNDPFASSDFPKTVTDIGIRDAGSHIQSMA-MSCPQTQRVLGGYSQGAIV 85
::: | ::| :

Qy 111 -----TAAVSSELGSAGEVKVGVALFG--YTQNLRGG--IANYP--RE 150
::: | ::| :
Db 86 AGYTSAVVPPAPVPQVAPEPAPEVANHVAAVTFLGPSAQFLGYGAPPATGLPYQP 145
::: | ::| :

Qy 151 RTKVFCNVGDVCTGTLLIITPAHLSVTIEAR-GEEAARFLRDRI 192
::: | ::| :
Db 146 KITLQCADGDSIC-DGNSPVAHLGYANGVMWGQGANFAASRL 187
::: | ::| :

RESULT 11

G70987

Probable cutinase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70987
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70987
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-174 <COL>
A;Cross-references: UNIPARC:UPI00000DSE96; GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CAN
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV1758
C;Superfamily: cutinase

| | Query Match | 9.8% | Score 98; | DB 2; | Length 174; |
|----------------------|-------------|-----------------|-----------|------------|-------------|
| Bst Local Similarity | 29.9%; | Pred. No. 0.14; | | | |
| Matches | 52; | Conservative | 22; | Mismatches | 64; |
| Gaps | Indels | 36; | Gaps | 12; | |

Qy 44 NGLESHEI--RNIIWGCVGPYDAALATNFLPRGTSQAANI-DEGRKLFALANOKCPNTPVV 100
::: | ::| :
Db 11 DALRSKI EKSGVGVDP-----ATTDFP--TAAGIYDAGTHVEOTA-ANCPOSKL V 62
::: | ::| :

Qy 101 AGGYSQGAALI-----AAAVSE-----LSGAVEQVKVGVALFGY--TONLNRRG-- 143
::: | ::| :
Db 63 LGFSOGAAVMGFVTTAAAI PDGAPI DAPRPMPPEVDHVAATFLFGMPSVFAMHSIGAPP 122
::: | ::| :

RESULT 10

QY 144 --TANYPRETKVFCNVDAVCT--GTLITPAHLSYTIARG-ARFLRDRI 192
Db 123 IVIGPLYAEKTIQICAGDPVPCSSGN---WAHNGYADGMVQQAFAAGRL 173

RESULT 12
F70887
hypothetical protein Rv3802c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: F70887
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70887
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-336 <COL>
A;Cross-references: UNIPROT:O53581; UNIPARC:UPI00000D1D1; GB:AL022076; GB:AL123456; NID
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv3802c

Query Match 9.6%; Score 96; DB 2; Length 336;
Best Local Similarity 22.4%; Pred. No. 0.46; Mismatches 24; Indels 66; Gaps 10;
Matches 50; Conservative 24

QY 16 ACPDAILIFARGSTE-----PGNMGITV-GPALANGLESHIRNIWQGVGGP 61
Db 71 SCDPQVMSVPGTWESPQONPLNPQFPKALLKVTGTAQAPARVQTYVAYTAQF 130

QY 62 YDAALATNLFPRGTSQANIDEGKRLFALA----NQKCPNTPVAGVYSGQAALIAAVSE 117
Db 131 HNPLTTDNQMSYNDRA---EGTRAMVAAMTMNRCPLTSYVLIGFSQGAIVAGDVASD 187

QY 118 LS---GAVKEQ-VKGVAFGYTQNLQNRGGIANY----- 147
Db 188 IGNRGFPVDEDLVLGVTLIADGRQO---GVGNQVPPSPRGEGABITLHEVPVLSGLGLT 244

QY 148 ---PRE-----RTKVFNCVGDVACTG-TLITPAHLSVTI 178
Db 245 MTGPRPGGFGALDGRITNEICAQGLICAAQAQAFSPANLPTTL 287

RESULT 13
T35575
hypothetical protein SC6G4.24 SC6G4.24 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35575
R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL data Library, August 1998
A;Reference number: Z21583
A;Accession: T35575
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-420 <SAU>
A;Cross-references: UNIPROT:O86787; UNIPARC:UPI00000DAD79; EMBL:AL031317; PIDN:CAA20402
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC6G4.24

Query Match 9.0%; Score 89.5; DB 2; Length 420;
Best Local Similarity 26.4%; Pred. No. 2.3; Mismatches 39; Indels 17; Gaps 6;
Matches 39; Conservative 22

QY 10 EGSACNACPDAILIFARGSPGNGMITVGPALAN-----GLSHIRNI-WIQGVGG 60

Db 105 EAG-ADPAPRRRLFRKAPAPVTVVVSHGYCLNQDSWHFQRAALRGVVRVVTWDQRSHG 163
QY 61 PYDAALATNLFPRGTSQANIDB-GKRLPALANQKCPNTPVAGVYSGQAALIAAAVSELS 119
Db 164 RSGRGVAQT---RDDRVPVSIIEGLRDLKAVIDAAAPEGPIVLVGHSMGGMTVMALADAFP 220

QY 120 GAVKEQVKGVAFGYTQNLQNRGGIANY 147
Db 221 DLVRRVVGVALVGTS---SGRLGEVNF 245

RESULT 14
E85557
enterobactin synthetase component EntF [similarity] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85557
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85557
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1293 <STO>
A;Cross-references: UNIPROT:Q8XBV9; UNIPARC:UPI0000129FD3; GB:AE005174; NID:G12513476; F
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: entF
C;Superfamily: enterobactin synthetase component F; acetate-CoA ligase homology; acyl
C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;1006/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 8.8%; Score 88; DB 2; Length 1293;
Best Local Similarity 24.7%; Pred. No. 12; Mismatches 57; Conservative 26; Indels 64; Gaps 13;
Matches 57

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPCNGMITVGPAL-----ANG-----LSS 48
Db 1037 KLAIIIDGDESSRRMGFETILPLREGN-----GPTLFCFHPASGFANQFVLSR 1086

QY 49 HIRNIW-IQGVGYPYDAALATNLFPRGTSQ---ANIDE--GKRLPALANQKCPNTPVAGG 103
Db 1087 YLDPLWSIIQISP-----RHPGPMQTATNLDEVCEHAHLATLLEQQ-PHGPYYLLG 1136

QY 104 YSQAALIAAAVSELGAVKEQVKGVAFG-----YTONLQNRGG-----TANYPRER- 151
Db 1137 YSLGTTLAQGIARLR-ARGEQVAFGLLDTWPPETONWQKEANGLDPEVLAEINRERE 1195

QY 152 -----TKVFCNVGDVACTGTLITPAHLSYTIARGEAARFLRDR 191
Db 1196 AFLAAQGSTSTELFTTIEGYNADVRLTLTAH---SVPDFGKATLFAER 1243

RESULT 15
A90707
enterobactin synthetase component EntF [imported] - Escherichia coli (strain O157:H7, s
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A90707
R;Havashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90707
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1293 <HAY>
A;Cross-references: UNIPROT:Q8XBV9; UNIPARC:UPI0000129FD3; GB:BA000007; PIDN:BA834048.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:

A:Gene: ECs0625
C:Superfamily: enterobactin synthetase component F; acetate-CoA ligase homology; acyl ca
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:1006/Binding site: phosphopantetheine (Ser) (covalent) #status Predicted

Query Match 8.8; Score 88; DB 2; Length 1293;
Best Local Similarity 24.7%; Pred. No. 12;
Matches 57; Conservative 26; Mismatches 84; Indels 64; Gaps 13;

QY 1 QLGAIEENGLESANACPDAILIFARGSTPEGNMGITVGPAL-----ANG-----LES 48
Db 1037 KLATIIDGEEDSRRMGFETILPLREGN-----GPTLCFCHPASGFANQPSVLSR 1086
QY 49 HIRNIW-IQVGGPYDAALATNPLPRGTSQ--ANIDE--GKRLFALANQKCPNTPVVAGG 103
Db 1087 YLDPLWSIIIGIQSF-----RPHGPMQTATNLDEVCEAHLATLLEQQ-PHGPYYLLG 1136
QY 104 YSGAALIAAAVSELSGAVKEQKGVALFG-----YTQNLQNRGG-----IANYPRER- 151
Db 1137 YSLGGTLAQGIARLR-ARGEQVAFGLGLDTPPETQNWQKEANGLDPEVLAEINRERE 1195
QY 152 -----TKVFCNVGDVCTGLIITPAHLSVTIEARGHAARFLDRD 191
Db 1196 AFLAAQGGSTSELTFTIEGNYADAVRLLTAAH---SVPDFGKATLFVAER 1243

Search completed: February 4, 2006, 04:57:00
Job time : 46 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:48:38 ; Search time 253 Seconds

(without alignments)

540.998 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPD.....SYTIERGEARFLRDRIIRA 194

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------|--------------------|
| 1 | 596 | 59.8 | 209 | 1 CUTI_ALTPR | P41744 alternaria |
| 2 | 595.5 | 59.8 | 228 | 2 Q52AU1_MAGGR | Q52au1 magnaporthe |
| 3 | 593.5 | 59.6 | 228 | 1 CUTI_MAGGR | P30272 magnaporthe |
| 4 | 576 | 57.8 | 224 | 1 CUTI_COLGL | P11373 colletotric |
| 5 | 576 | 57.8 | 227 | 2 Q41I88_GIBZE | Q41i88 gibberella |
| 6 | 575 | 57.7 | 248 | 2 Q41KB6_GIBZE | Q41kb6 gibberella |
| 7 | 564 | 56.6 | 223 | 1 CUTI_ASCRA | P29292 ascochyta r |
| 8 | 550.5 | 55.3 | 228 | 1 CUTI_COLCA | P10951 colletotric |
| 9 | 550 | 55.2 | 230 | 1 CUTI_FUSSC | Q99174 fusarium so |
| 10 | 545 | 54.7 | 230 | 1 CUTI1_FUSSO | P00590 fusarium so |
| 11 | 543.5 | 54.6 | 231 | 2 Q41H51_GIBZE | Q41h51 gibberella |
| 12 | 542.5 | 54.5 | 231 | 1 CUTI2_FUSSO | Q96ut0 fusarium so |
| 13 | 540.5 | 54.3 | 231 | 1 CUTI3_FUSSO | Q96u89 fusarium so |
| 14 | 494 | 49.6 | 217 | 2 Q4W924_ASPFU | Q4w924 aspergillus |
| 15 | 467.5 | 46.9 | 214 | 2 Q4WQ22_ASPFU | Q4wq22 aspergillus |
| 16 | 465.5 | 46.7 | 213 | 2 Q5B2C1_EMENI | Q5bx00 aspergillus |
| 17 | 463.5 | 46.5 | 221 | 2 Q5AX00_EMENI | Q5ax00 aspergillus |
| 18 | 458 | 46.0 | 211 | 2 Q4X1N0_ASPFU | Q4x1n0 aspergillus |
| 19 | 450 | 45.2 | 213 | 1 CUTI_ASPOR | P52956 aspergillus |
| 20 | 444 | 44.6 | 257 | 2 Q5AV79_EMENI | Q5av79 aspergillus |
| 21 | 412.5 | 41.4 | 228 | 2 Q51N02_MAGGR | Q51nu2 magnaporthe |
| 22 | 329 | 33.0 | 214 | 2 Q51KM8_MAGGR | Q51km8 magnaporthe |
| 23 | 311 | 31.2 | 230 | 2 Q4HWM4_GIBZE | Q4hwm4 gibberella |
| 24 | 269 | 27.0 | 427 | 2 Q4IM18_GIBZE | Q4im18 gibberella |
| 25 | 262 | 26.3 | 254 | 2 Q9P960_ASPOR | Q9p960 aspergillus |
| 26 | 242.5 | 24.3 | 686 | 2 Q5B9E7_EMENI | Q5b9e7 aspergillus |
| 27 | 241.5 | 24.2 | 375 | 2 Q4X078_ASPFU | Q4x078 aspergillus |
| 28 | 240.5 | 24.1 | 216 | 2 Q52018_MAGGR | Q52018 magnaporthe |
| 29 | 236 | 23.7 | 234 | 2 Q529T3_MAGGR | Q529t3 magnaporthe |
| 30 | 234.5 | 23.5 | 1003 | 2 Q51V73_MAGGR | Q51v73 magnaporthe |
| 31 | 229.5 | 23.0 | 201 | 1 CUTI_MONFR | Q8tgb8 monilinia f |

| | | | | | |
|----|-------|------|-----|----------------|--------------------|
| 32 | 228 | 22.9 | 202 | 1 CUTI_BOTCI | Q00298 botrytis ci |
| 33 | 222.5 | 22.3 | 203 | 1 CUTI_PYBR | Q9Y7g8 pyrenopeziz |
| 34 | 220 | 22.1 | 190 | 2 Q51H99_MAGGR | Q51h99 magnaporthe |
| 35 | 206.5 | 20.7 | 287 | 2 Q529U1_MAGGR | Q529j1 magnaporthe |
| 36 | 205.5 | 20.6 | 236 | 1 CUTI_ERYGR | Q8xlp1 erysiph gr |
| 37 | 195 | 19.6 | 217 | 2 Q58G92_PHYIN | Q58g92 phytophthor |
| 38 | 193 | 19.4 | 211 | 2 Q73S40_MYCPA | Q73s40 mycobacteri |
| 39 | 189.5 | 19.0 | 217 | 1 CUT1_MYCBO | P63880 mycobacteri |
| 40 | 189.5 | 19.0 | 217 | 1 CUT1_MYCTU | P63879 mycobacteri |
| 41 | 186.5 | 18.9 | 230 | 1 CUT2_MYCTU | P63882 mycobacteri |
| 42 | 186.5 | 18.9 | 639 | 2 Q4P198_USTMA | P4p198 ustilago ma |
| 43 | 187.5 | 18.8 | 230 | 2 Q4P198_USTMA | P4p198 ustilago ma |
| 44 | 182 | 18.3 | 234 | 2 Q73ZX5_MYCPA | Q73zx5 mycobacteri |
| 45 | 181.5 | 18.2 | 235 | 2 Q73UE0_MYCPA | Q73ue0 mycobacteri |

ALIGNMENTS

RESULT 1

| ID | CUTI_ALTPR | STANDARD; | PRT; | 209 AA. |
|----|--|-----------|------|---------|
| AC | P41744; | | | |
| DT | 01-NOV-1995 (Rel. 32, Created) | | | |
| DT | 01-NOV-1995 (Rel. 32, Last sequence update) | | | |
| DT | 10-MAY-2005 (Rel. 47, Last annotation update) | | | |
| DE | Cutinase precursor (BC 3.1.1.74) (Cutin hydrolase). | | | |
| GN | Name=CUTAB1; | | | |
| OS | Alternaria brassicicola. | | | |
| OC | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; | | | |
| OC | Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria. | | | |
| OX | NCBI_TaxID=29001; | | | |
| RP | [1] | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RA | Yao C., Koeller W.; | | | |
| RL | Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases. | | | |
| CC | -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that | | | |
| CC | penetrates through the cuticular barrier into the host plant during | | | |
| CC | the initial stage of the fungal infection (By similarity). | | | |
| CC | -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers. | | | |
| CC | -1- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -1- SIMILARITY: Belongs to the cutinase family. | | | |
| CC | ----- | | | |
| CC | This Swiss-Prot entry is copyright. It is produced through a collaboration | | | |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - | | | |
| CC | the European Bioinformatics Institute. There are no restrictions on its | | | |
| CC | use as long as its content is in no way modified and this statement is not | | | |
| CC | removed. | | | |
| CC | ----- | | | |
| CC | EMBL; U03393; AAA03470.1; -; Unassigned_RNA. | | | |
| DR | HSSP; P00590; 1XZG. | | | |
| DR | InterPro; IPR000675; Cutinase. | | | |
| DR | InterPro; IPR01150; Cutinase_monf. | | | |
| DR | Pfam; PF01083; Cutinase; 1. | | | |
| DR | PIRSF; PIRSF000861; Cutinase; 1. | | | |
| DR | PRINTS; PR00129; CUTINASE. | | | |
| DR | PROSITE; PS00155; CUTINASE_1; 1. | | | |
| DR | PROSITE; PS00933; CUTINASE_2; 1. | | | |
| KW | Hydrolase; Serine esterase; Signal. | | | |
| FT | SIGNAL 1 ? Potential. | | | |
| FT | CHAIN ? 209 | | | |
| FT | ACT_SITE 119 174 | | | |
| FT | ACT_SITE 174 174 | | | |
| FT | ACT_SITE 187 174 | | | |
| FT | ACT_SITE 187 174 | | | |
| FT | DISULFID 29 177 | | | |
| FT | DISULFID 108 170 | | | |
| SQ | SEQUENCE 209 AA; 21649 MW; 1756D06D84093A64 CRC64; | | | |

Query Match 59.8%; Score 596; DB 1; Length 209;

Best Local Similarity 60.3%; Pred. No. 5.1e-43;

Matches 117; Conservative 22; Mismatches 53; Indels 2; Gaps 1;

QY 1 QLGAIENGLESANACPDAILIFARGSTEGNMGITVGPALANGLES--HINIWIQGV 58
 DB 13 QASTTRNELETGSSDACPRITIFARGSTEGNMGALVGPFTANALLESAYGASNVWQGV 72
 QY 59 GGPYDAALATNPLPRTGTSOANIIDEGRKLFALANOKCPNTPVAVAGGYSQGAALIAAAVSEL 118
 DB 73 GGPYTAGLVENALPAGTSQAIREAORLFWLAASKCPNTPITAGGYSQGANVMSNAIPGL 132
 QY 119 SGAVKEQVKGVALFGYTONLQNRGGIANYPRERTKVCNVGDVAVCTGTLLIITPAHLSYTI 178
 DB 133 SAAVQDIQGVVLFYGTKNLQNGRIPNPTSTKTYICVETGDLVCGNLTLLIITPAHLSYD 192
 QY 179 EARGEAAARFLDRRI 192
 DB 193 EAAVQAPTFLRAQI 206

RESULT 2
 Q52AUI_MAGGR PRELIMINARY; PRT; 228 AA.
 AC Q52AUI;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNAMES=MG01943.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachi H., Ambruster J., Bachansang P., Baldwin J., Barry A.,
 RA Bayul T., Blitshstein B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dejee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Huby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvasselis M., Karlsson B.,
 RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., McGhee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Plunkhug P., Piquani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settupalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
 RA Towey S., Taamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea."
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AACU01000378; EAA53958.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 228 AA; 24191 MW; 36BF2F253B8F7709 CRC64;

Query Match 59.8%; Score 595.5; DB 2; Length 228;
 Best Local Similarity 59.5%; Pred. No. 6.2e-43;
 Matches 116; Conservative 27; Mismatches 51; Indels 1; Gaps 1;

QY 1 QLGAIENGLESANACPDAILIFARGSTEGNMGITVGPALANGLES--HINIWIQGV 59
 DB 33 QLSVNRNDLISGNAACPSVILIFARASGEVGNMGLSAGTNVASALEREFRNDIWWQGVG 92
 QY 60 GPYDAALATNPLPRTGTSOANIIDEGRKLFALANOKCPNTPVAVAGGYSQGAALIAAAVSEL 119
 DB 93 DPYDAALSPNPLPAGTTQGAIDEAKRMFTLANTKCPNAAVVAGGYSQGTAVMFAVSEMP 152
 QY 120 GAVKEQVKGVALFGYTONLQNRGGIANYPRERTKVCNVGDVAVCTGTLLIITPAHLSYTI 179
 DB 153 AAVQDIQGVVLFYGTKNLQNGRIPDPTTEKTEVICNASDAVCPGTLLIITPAHLSYTI 212
 QY 180 EARGEAAARFLDRRI 194
 DB 213 SSIAAPNWLIRQIRA 227

RESULT 3
 ID CUTI_MAGGR STANDARD; PRT; 228 AA.
 AC P30272;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DB Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
 GN Name=CUTI;
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=148305;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=4091-S-8;
 RC MEDLINE=92212279; PubMed=1557023;
 RX Sweigard J.A., Chumley F., Valent B.;
 RA "Cloning and analysis of CUT1, a cutinase gene from Magnaporthe
 grisea.";
 RT Mol. Gen. Genet. 232:174-182(1992).
 RL -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
 forms the structure of plant cuticle. Allows pathogenic fungi to
 penetrate through the cuticular barrier into the host plant during
 the initial stage of the fungal infection.
 CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the cutinase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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 removed.


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RC STRAIN-PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepele Y., Collamore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Maucelli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM01000142; EAA72390.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 23525 MW; 9F57BE86176C1595 CRC64;

Query Match 57.8%; Score 576; DB 2; Length 227;
Best Local Similarity 58.9%; Pred. No. 2.9e-41;
Matches 116; Conservative 27; Mismatches 50; Indels 4; Gaps 3;

QY 1 QLGAI-ENGLESGSANACPDAILIFARGSTPEPNMGITVGPALANGLESHI--RNIIWQIG 57
DB 30 QAGSITRNDLSSGASSACPPVIFVARGSTELNGL-TLGPVSALESYGRDKVWQIG 88
QY 58 VGGPYDAALATNPLPRTGTOANIDEGRKLPALANQKCPNTPVWAGYSQGAALIAAVSE 117
DB 89 VGGAYDATIGDNLPRGTSAARIREMIALFNLANSKPCSAKVWAGYSQGAALAAASIED 148
QY 118 LSGAVKEOVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGLTIITPAHLSY 177
DB 149 LSTSVNRDKVVGTVLFGYTKNQLNGLRIPNYPRTKVFNCVGDVAVCTGLTIITPAHLSY 208
QY 178 IEARGEAAARFLDRIRA 194
DB 209 SDASGAPAEFLIQRVAA 225

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RESULT 6
Q4IKB6 GIBZE PRELIMINARY; PRT; 248 AA.
AC Q4IKB6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG02342.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OC NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepele Y., Collamore A., Cook A., Cooke P., Corum B., Dearellano K.,

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RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Maucelli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM01000116; EAA69882.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 248 AA; 24742 MW; 24CEB193712F698F CRC64;

Query Match 57.7%; Score 575; DB 2; Length 248;
Best Local Similarity 56.2%; Pred. No. 3.9e-41;
Matches 108; Conservative 31; Mismatches 51; Indels 2; Gaps 1;

QY 3 GAIENGLESGSANACPDAILIFARGSTPEPNMGITVGPALANGLESHI--RNIIWQVGG 60
DB 56 GSTRNDLEQGAAGSCPKAIFARATTEQGNMGMTGTPAVASKLEAKYCKGGVWVQVGG 115
QY 61 PYDAALATNPLPRTGTOANIDEGRKLPALANQKCPNTPVWAGYSQGAALIAAVSELGG 120
DB 116 PYTADVGNLMPDGSPPAGINEAVRLNMAHEKCPDTPVVTGGYSQGTALVAAASKLDLP 175
QY 121 AVKEOVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGLTIITPAHLSY 180
DB 176 KVMQVQKGVCLFGYTKNAQNEALPNPKORTAICNVGDVAVCTGLTIITPAHLSY 235
QY 181 RGEAAARFLDRIRI 192
DB 236 AGAPEFLISKI 247

RESULT 7
CUTI_ASCRA STANDARD; PRT; 223 AA.
AC P29292;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
GN Name=CUT;
OS Ascochyta rabiei (Chickpea ascochyta blight fungus) (Didymella
OS rabiei).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothromycetes incertae sedis;
OC Mycosphaerellaceae; Mycosphaerella.
OC NCBI_TaxID=5454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CHS 534.65;
RA Tenhaken R., Barz W.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection (By similarity).
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- SIMILARITY: Belongs to the cutinase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X65628; CAA46582.1; -; Genomic_DNA.
CC PIR; S21427; S21427.
CC HSP; P00590; 1CUW.
CC InterPro; IPR000675; Cutinase.
CC InterPro; IPR011150; Cutinase_monf.
CC Pfam; PF01083; Cutinase; 1.
CC PIRSF; PIRSF000861; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE_1; 1.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC K1 Hydroxylase; Serine esterase; Signal.
CC FT SIGNAL 1 19 Potential.
CC CHAIN 20 223 Cutinase.
CC ACT_SITE 135 135 By similarity.
CC ACT_SITE 189 189 By similarity.
CC ACT_SITE 202 202 By similarity.
CC DISULFID 46 192 By similarity.
CC DISULFID 124 185 By similarity.
CC SEQUENCE 223 AA; 1882A5ADD1B5E7FB CRC64;

Query Match 56.6%; Score 564; DB 1; Length 223;
Best Local Similarity 58.6%; Pred. No. 3e-40;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

Qy 5 IENGLESGSNACPDAILLIFARGSTPEGNIGITVGPALANGLESH--IRNIWIOGVGSPYD 63
Db 34 IRSELEQSSSCPKAILLIFARGSTPEGNIGITVGPALANGLESH--IRNIWIOGVGSPYD 93

Qy 64 AALATNFPRTGTOANIDEKRLFALANOKPNTVPVAGVSGQAALIAAAVSELGAVK 123
Db 94 ADLPNFPDGTQSQAINAEVRLFNEANTKCPSTPIVAGVSGQTAVMAGAI PKLD-AVR 152

Qy 124 EQVKGVALFGYTONLQNRGGIANYPRERTKVFNCNVGDAVCTGTLLIITPAHLSYTYEARGE 183
Db 153 ARVVGTVLFGYTONQNNKGIKDPQEDLQVYCEVGLVCDGTLLIITVSHFLYLEAAGP 212

Qy 184 AARFLDRIRA 194
Db 213 APEFLKSKIGA 223

RESULT 8
CUTI_COLCA STANDARD; PRT; 228 AA.
AC P10951;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
GN Name=CUTA;
OS Colletotrichum capsici (Anthracnose fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Mitosporic Phyllachoraceae; Colletotrichum.
OX NCBI_TaxID=5456;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC STRAIN=ATCC 48574;
RA Ettinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid sequence
RT from phytopathogenic fungi."
RL Biochemistry 26:7883-7892(1987).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that

```

```

CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- PM: The 2 disulfide bonds play a critical role in holding the
CC catalytic residues in juxta-position; reduction of the disulfide
CC bridges results in the complete inactivation of the enzyme.
CC -!- SIMILARITY: Belongs to the cutinase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M18033; AAA33043.1; -; Genomic_DNA.
CC PIR; A27451; A27451.
CC HSP; P00590; 1CUW.
CC InterPro; IPR000675; Cutinase.
CC InterPro; IPR011150; Cutinase_monf.
CC Pfam; PF01083; Cutinase; 1.
CC PIRSF; PIRSF000861; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE_1; 1.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC K1 Direct protein sequencing; Hydrolase; Serine esterase; Signal.
CC FT SIGNAL 1 16 Potential.
CC CHAIN 17 228 Cutinase.
CC ACT_SITE 140 140 By similarity.
CC ACT_SITE 195 195 By similarity.
CC ACT_SITE 208 208 By similarity.
CC DISULFID 49 198 By similarity.
CC DISULFID 129 191 By similarity.
CC SEQUENCE 228 AA; 23714 MW; 3825D42C23DA139B CRC64;

Query Match 55.3%; Score 550.5; DB 1; Length 228;
Best Local Similarity 57.1%; Pred. No. 4.5e-39;
Matches 108; Conservative 27; Mismatches 51; Indels 3; Gaps 2;

Qy 7 NLESGSANACPDAILLIFARGSTPEGNIGITVGPALANGLESH--IRNIWIOGVGSPYD 64
Db 39 NELESGSSNCPKVIYIFARASTPEGNIGISAGPIVADALESRYGASQVWVQGVGSPYSA 98

Qy 65 AALATNF-LPRGTSQANIDEKRLFALANOKPNTVPVAGVSGQAALIAAAVSELGAVK 123
Db 99 DLASNFIPEGTSRVAINAKRLFLTANTKCPNSAVVAGVSGQTAVNASSISELSSTIQ 158

Qy 124 EQVKGVALFGYTONLQNRGGIANYPRERTKVFNCNVGDAVCTGTLLIITPAHLSYTYEARGE 183
Db 159 NQIKGVVLSAITKNLQNLGRIPNFTSKTEVYCALADAVCYGTLLIIPAHFLYQADAATS 218

Qy 184 AARFLDRIRI 192
Db 219 APRFLAARI 227

RESULT 9
CUTI_FUSSC STANDARD; PRT; 230 AA.
AC Q99174;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
GN Name=CUTA;
OS Fusarium solani subsp. cucurbitae (Nectria ipomoeae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=57162;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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```

RC STRAIN=PCB 153;
RX MEDLINE=97254998; PubMed=9100380;
RA Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M.,
RA Rees-George J., Rikkerink E.H., Templeton M.D.;
RT "Effect of disruption of a cutinase gene (cutA) on virulence and
RT tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward
RT Cucurbita maxima and C. moschata.";
RL Mol. Plant Microbe Interact. 10:355-368(1997).
CC -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the cutinase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U63335; AAB05922.1; -; Genomic_DNA.
CC DR HSP; P00590; 2CUT.
CC DR SMR; Q99174; 33-229.
CC DR InterPro; IPR000675; Cutinase.
CC DR InterPro; IPR011150; Cutinase_monof.
CC DR Pfam; PF01083; Cutinase; 1.
CC DR PIRSF; PIRSF000861; Cutinase; 1.
CC DR PRINTS; PR00129; CUTINASE.
CC DR PROSITE; PS00155; CUTINASE_1; 1.
CC DR PROSITE; PS00931; CUTINASE_2; 1.
CC DR Hydrolyase; Serine esterase; Signal.
CC KW SIGNAL 1 16 By similarity.
CC FT CHAIN 17 230 Cutinase.
CC FT ACT_SITE 136 136 By similarity.
CC FT ACT_SITE 191 191 By similarity.
CC FT ACT_SITE 204 204 By similarity.
CC FT DISULFID 47 194 By similarity.
CC FT DISULFID 125 187 By similarity.
CC SQ SEQUENCE 230 AA; 23902 MW; 05FB3C33326405AA CRC64;
CC -----
Query Match 55.2%; Score 550; DB 1; Length 230;
Best Local Similarity 55.3%; Pred. No. 5e-39;
Matches 109; Conservative 32; Mismatches 52; Indels 4; Gaps 3;

QY 1 QLG-ATENGLESANACPDAILIFARGSTEPGNWGITVGPALANGLESHI--RNTWIOG 57
DB 30 QLGRTTRDDLLNGNSACDVIYIARGSTETGNLG-TLGPSTASNLSEAFGTGQVWIOG 88
QY 58 VCGPYDAALATNFPRGTSQANTDEGKRLPALANQKCPNTPVAGGYSQGAALIAAAVSE 117
DB 89 VGYAYRATLGDNALPRGTSAAATREMLGLFQQAATKCPDATINGGYSQGAALAAASIED 148
QY 118 LSGAVKEQVGKVALFGYTONLQNRGGIANYPRERTKVCNVGDVACTGTLLIIPAHLSYLT 177
DB 149 LDSAIRDKIAGTVLFGYTKLQNRGRIPNYPADRTKVCNVGDLVCTGSLIVAAPHLAYG 208
QY 178 IEARGENARFLDRIRA 194
DB 209 PDARGPAPEFLIEKVR 225

RESULT 10
CUTIL_FUSSO STANDARD; PRT; 230 AA.
ID CUTIL_FUSSO
AC P00590;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cutinase 1 precursor (EC 3.1.1.74) (Cutin hydrolase 1).
GN Name=CUT1; Synonyms=CUTA;
OS Fusarium solani subsp. pisii (Nectria haematococca).

```

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
[1]
NCBI_TaxID=70791;
RN NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC STRAIN=T-8;
RA Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.;
RT "Cloning and structure determination of cDNA for cutinase, an enzyme
involved in fungal penetration of plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=89197761; PubMed=2703464;
RX Soliday C.L., Dickman M.B., Kolattukudy P.E.;
RT "Structure of the cutinase gene and detection of promoter activity in
the 5'-flanking region by fungal transformation.";
RL J. Bacteriol. 171:1942-1951(1989).
[3]
RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RP MEDLINE=92220194; PubMed=1560844; DOI=10.1038/356615a0;
RX Martinez C., de Geus P., Lauwers M., Matthysens G., Cambillau C.;
RA "Fusarium solani cutinase is a lipolytic enzyme with a catalytic
serine accessible to solvent.";
RT Nature 356:615-618(1992).
[4]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RP MEDLINE=94114517; PubMed=8286366;
RX Martinez C., Nicolas A., van Tilbeurgh H., Egloff M.-P., Cudrey C.,
RA Verger R., Cambillau C.;
RT "Cutinase, a lipolytic enzyme with a preformed oxyanion hole.";
RL Biochemistry 33:83-89(1994).
[5]
RN X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS).
RP MEDLINE=97318923; PubMed=9175860; DOI=10.1006/jmbi.1997.1000;
RX Longhi S., Czjzek M., Lamzin V., Nicolas A., Cambillau C.;
RA "Atomic resolution (1.0 A) crystal structure of *Fusarium solani*
cutinase: stereochemical analysis.";
RT J. Mol. Biol. 268:779-799(1997).
[6]
RN X-RAY CRYSTALLOGRAPHY (1.15 ANGSTROMS) OF 33-230.
RP Nicolas A., Martinez C., Cambillau C.;
RL Submitted (MAR-1997) to the PDB data bank.
[7]
RN STRUCTURE BY NMR.
RP MEDLINE=98046750; PubMed=9385640;
RX Prompers J.J., Groenewegen A., van Schaik R.C., Pepermans H.A.M.,
RA Hilbers C.W.;
RT "1H, 13C, and 15N resonance assignments of *Fusarium solani* pisi
cutinase and preliminary features of the structure in solution.";
RL Protein Sci. 6:2375-2384(1997).
CC -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
forms the structure of plant cuticle. Allows pathogenic fungi to
penetrate through the cuticular barrier into the host plant during
the initial stage of the fungal infection.
CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PMTM: The 2 disulfide bonds play a critical role in holding the
catalytic residues in juxta-position; reduction of the disulfide
bridges results in the complete inactivation of the enzyme.
CC -1- SIMILARITY: Belongs to the cutinase family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; K02640; AAA33334.1; -; mRNA.
DR EMBL; M29759; AAA33335.1; -; Genomic_DNA.
DR PIR; A32836; UVFUS.
DR PDB; 1AGY; X-ray; @=31-230.
DR PDB; 1CEX; X-ray; @=17-230.

```
RA Vassiliev H., Venkataranan V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RL "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM01000159; BAA71659.1; -; Genomic_DNA.
SQ SEQUENCE 231 AA; 23544 MW; 675D6B3853E092C2 CRC64;

Query Match 54.6%; Score 543.5; DB 2; Length 231;
Best Local Similarity 57.4%; Pred. No. 1.8e-38;
Matches 108; Conservative 29; Mismatches 48; Indels 3; Gaps 3;

QY 3 GAIENGLESGSANACPDAILIFARGSTEPGNGITVGPALANGLES-HIRN-TWIOGVGG 60
DB | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
32 GSTRNDLKNNGSGCPGVIFVARGSTETGNLG-TLGPVRVSALESKYGRNGVWIOGVGG 90

QY 61 PYDAALATNPLPRGTSQANIDEKRLFALANOKCPNTPVVAGYSQGAALIAAAVSELGS 120
DB | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
91 ATTAGVGENALPRGTYTAAIREMVGHENDANQKCPNAVIVAGYSQGAALAAAATVDVA 150

QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGTLITPAHLSYTTIEA 180
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
151 GIREKIAGTVLFGYTKNLQNRGKIPSPYEDRTKVCNVDGAVCTGTLITPAHLSYTTIEA 210

QY 181 RGEAARPL 188
DB | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 SGAARPL 218

RESULT 12
CUT12_FUSO STANDARD; PRT; 231 AA.
ID CUT12_FUSO STANDARD; PRT; 231 AA.
AC Q96UT0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cutinase 2 precursor (EC 3.1.1.74) (Cutin hydrolase 2).
GN Name=CUT2;
OS Fusarium solani subsp. pisi (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T-8;
RX MEDLINE=21864232; PubMed=11756444; DOI=10.1074/jbc.M108799200;
RA Li D., Sirakova T., Rogers L., Ettinger W.F., Kolattukudy P.E.;
RT "Regulation of constitutively expressed and induced cutinase genes by
RT different zinc finger transcription factors in Fusarium solani f. sp.
RL J. Biol. Chem. 277:7905-7912(2002).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection (By similarity).
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the cutinase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF417004; AAL18696.1; -; Genomic_DNA.
DR HSSP; P00590; 2CUT.
DR SNR; Q96UT0; 35-230.
DR InterPro; IPR000675; Cutinase.
```

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DR InterPro; IPR011150; Cutinase_monf.
DR Pfam; PF01083; Cutinase; 1.
DR FIRSF; FIRSF00861; Cutinase; 1.
DR PRINTS; PR00129; CUTINASE.
DR PROSITE; PS00155; CUTINASE 1; 1.
DR PROSITE; PS00931; CUTINASE 2; 1.
KW Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 231 Cutinase 2.
FT ACT_SITE 137 137 By similarity.
FT ACT_SITE 192 192 By similarity.
FT ACT_SITE 205 205 By similarity.
FT DISULFID 48 195 By similarity.
FT DISULFID 126 188 By similarity.
SQ SEQUENCE 231 AA; 23932 MW; 8047714A249CB756 CRC64;

Query Match 54.5%; Score 542.5; DB 1; Length 231;
Best Local Similarity 55.2%; Pred. No. 2.2e-38;
Matches 107; Conservative 30; Mismatches 54; Indels 3; Gaps 2;

QY 3 GAIENGLESGSANACPDAILIFARGSTEPGNGITVGPALANGLESHI--RNWIOGVGG 60
DB | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 GTTRNDLTNGNSASCADVIFVARGSTETGNLG-TLGPSTASKLESAPGRDGVWIOGVGG 92

QY 61 PYDAALATNPLPRGTSQANIDEKRLFALANOKCPNTPVVAGYSQGAALIAAAVSELGS 120
DB | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 AYRATLGDNSLPRGTSAAIREMLGLPQQAATKCPDATLIAGGYSQGAALGAASVEDLDS 152

QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGTLITPAHLSYTTIEA 180
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 AIRDKIAGTVLFGYTKNLQNRGIPNPADRTKVCNTGDLVCTGSLIIAAPHLYTGPD 212

QY 181 RGEAARFLDRIRA 194
DB | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
213 RGPAPREFLIEKVR 226

RESULT 13
CUT13_FUSO STANDARD; PRT; 231 AA.
ID CUT13_FUSO STANDARD; PRT; 231 AA.
AC Q96US9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cutinase 3 precursor (EC 3.1.1.74) (Cutin hydrolase 3).
GN Name=CUT3;
OS Fusarium solani subsp. pisi (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T-8;
RX MEDLINE=21864232; PubMed=11756444; DOI=10.1074/jbc.M108799200;
RA Li D., Sirakova T., Rogers L., Ettinger W.F., Kolattukudy P.E.;
RT "Regulation of constitutively expressed and induced cutinase genes by
RT different zinc finger transcription factors in Fusarium solani f. sp.
RL J. Biol. Chem. 277:7905-7912(2002).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection (By similarity).
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the cutinase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF417004; AAL18696.1; -; Genomic_DNA.
DR HSSP; P00590; 2CUT.
DR SNR; Q96UT0; 35-230.
DR InterPro; IPR000675; Cutinase.
```

EMBL; AF417005; AAL18697.1; -; Genomic_DNA.
 DR HSSP; P00590; 2CUT.
 DR SMR; Q96US9; 35-230.
 DR InterPro; IPR000675; Cutinase.
 DR InterPro; IPR011150; Cutinase_monf.
 DR Pfam; PF01083; Cutinase; 1.
 DR Pfam; PF000861; Cutinase; 1.
 DR PRINTS; PRS000861; CUTINASE 1.
 DR PROSITE; PS00155; CUTINASE 1; 1.
 DR PROSITE; PS00931; CUTINASE 2; 1.
 DR KEGG; K01000; Serine esterase; Signal.
 KW Hydroxylase; Serine esterase; Signal.
 FT SIGNAL 1 16 Potential.
 FT CHAIN 17 231 Cutinase 3.
 FT ACT SITE 137 137 By similarity.
 FT ACT SITE 192 192 By similarity.
 FT ACT SITE 205 205 By similarity.
 FT ACT SITE 205 205 By similarity.
 FT DISULFID 48 195 By similarity.
 FT DISULFID 126 188 By similarity.
 FT DISULFID 126 188 By similarity.
 SQ SEQUENCE 231 AA; 24016 MW; DB39E3EECEDD202 CRC64;
 Query Match 54.3%; Score 540.5; DB 1; Length 231;
 Best Local Similarity 54.6%; Pred. No. 3.e-38;
 Matches 106; Conservative 30; Mismatches 55; Indels 3; Gaps 2;
 QY 3 GATENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHEI--RNIIWQGVGG 60
 DB 34 GTTRNDLTNGNSASCADVIFIVARGSTETGNLG-TLGPSTIASKLSAFGRDGVWIIQGVGG 92
 QY 61 PYDAALATNLFPRGTQANIDEGKRLPALANQKCPNTPVVGYSQGAALIAAAVSELG 120
 DB 93 AYRATIGDNLSPRGTSAAIREMLGIFQFPNTKCPDATTIANGYSQGAALAAVSEDEDS 152
 QY 121 AVKEQVKGVALFGYTNQLNQRGGIANYPRRTKVFNCVGDVACTGTGLIITPAHLSYTTIEA 180
 DB 153 AIRDKTAGTVLFGYTNQLNQRGGIANYPRRTKVFNCVGDVACTGTGLIITPAHLSYTTIEA 212
 QY 181 RGEAARFLDRIRA 194
 DB 213 RGPAPFLIEKVR 226
 RESULT 14
 Q4W924 ASPFU PRELIMINARY; PRT; 217 AA.
 ID Q4W924 ASPFU PRELIMINARY; PRT; 217 AA.
 AC Q4W924;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Cutinase, putative.
 OS ORFNames=Afu4903210;
 GN Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OC NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293;
 RA Niernan W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foerker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.;
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 Aspergillus fumigatus.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AAF01000016; EAL844469.1; -; Genomic DNA.
 SQ SEQUENCE 217 AA; 22483 MW; 10735C585B7690FA CRC64;
 Query Match 49.6%; Score 494; DB 2; Length 217;
 Best Local Similarity 50.8%; Pred. No. 3.e-34;
 Matches 98; Conservative 35; Mismatches 54; Indels 6; Gaps 3;
 QY 3 GATENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHEIRN--TWIQGVGG 60
 DB 28 GMSNELESG---PCRDVTTFARGSTEQGNMGLIVGVCSSLKDDLGSKVACQGVGG 84
 QY 61 PYDAALATNLFPRGTQANIDEGKRLPALANQKCPNTPVVGYSQGAALIAAAVSELG 120
 DB 85 AYTAQLAPNLSQNTNQASINAATDMFLATKCPNTKI VAGYSQGSVAIDNTIQA LGS 144
 QY 121 AVKEQVKGVALFGYTNQLNQRGGIANYPRRTKVFNCVGDVACTGTGLIITPAHLSYTTIEA 180
 DB 145 DLKAKVGGVVLFGFTRNVADKGGIIPGPKDQTKIYCAVGMVCVNTLIITPAHLTYGADA 204
 QY 181 RGEAARFLDRIR 193
 DB 205 -GDAAKFLASKVQ 216
 RESULT 15
 Q4WQV2 ASPFU PRELIMINARY; PRT; 214 AA.
 ID Q4WQV2 ASPFU PRELIMINARY; PRT; 214 AA.
 AC Q4WQV2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Cutinase, putative.
 OS ORFNames=Afu4914120;
 GN Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OC NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293;
 RA Niernan W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foerker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.;
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 Aspergillus fumigatus.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.


```
CC      preliminary data.
DR      EMBL; AAHF01000005; EAL89382.1; -; Genomic DNA.
SQ      SEQUENCE 214 AA; 22325 MW;  C0B300C69C56CB63 CRC64;

      Query Match      46.9%; Score 467.5; DB 2; Length 214;
      Best Local Similarity 49.7%; Pred. No. 5.5e-32;
      Matches 96; Conservative 30; Mismatches 62; Indels 5; Gaps 3;

QY      6 ENLESGSA---NACPDAILIIFARGSTFPGNMGITVGPALANGLE-SHIRNIWIQVGGP 61
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      23 ERLSSGNELRNGACKPITFIIFARASTFGLMGLSTGPAVCNSLKAAPQVACQGVGPA 82
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      62 YDAALATNFIPLRGTSQANTDEGKRLPALANQKCPNTPVWAGYSQGAALIAAAVSELGA 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      83 YTADLASNALPENTSOAINEAMELFQAASKCPDTQIVAGGYSQGTAVMDGSIKRLPEE 142
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      122 VKEQVKGVALFGVTQNLQNRGGIANYPREBTKVFCNVGDVAVCTGTLIITPAHLSYTIAR 181
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      143 VKERINGVVLFGYTRNAQERGQIANPPKOKKIYCAWGDVLCVCDGTLIIVTAHFTYGANT- 201
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      182 GEAARFLRDRIRA 194
      | | | | | | | | | |
Db      202 GDAARFLLGKLT 214
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Search completed: February 4, 2006, 04:56:11
Job time : 256 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2006, 04:56:24 ; Search time 48 Seconds
(without alignments)
334.148 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPDPA.....SYTIARGEARFLRDRIRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/prodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/prodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/prodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 991 | 99.5 | 194 | 2 | US-09-873-075A-1 |
| 2 | 991 | 99.5 | 229 | 1 | US-08-817-997A-2 |
| 3 | 500.5 | 50.3 | 231 | 2 | US-09-177-234-3 |
| 4 | 499.5 | 50.2 | 232 | 2 | US-09-177-234-8 |
| 5 | 482 | 48.4 | 232 | 2 | US-09-177-234-6 |
| 6 | 260 | 26.1 | 255 | 2 | US-09-585-468-1 |
| 7 | 260 | 26.1 | 255 | 2 | US-10-114-115A-1 |
| 8 | 260 | 26.1 | 255 | 2 | US-10-114-116-1 |
| 9 | 260 | 26.1 | 255 | 2 | US-10-231-478-1 |
| 10 | 189.5 | 19.0 | 217 | 2 | US-09-050-739-10 |
| 11 | 188.5 | 18.9 | 219 | 2 | US-09-050-739-14 |
| 12 | 178 | 17.9 | 226 | 2 | US-09-050-739-52 |
| 13 | 167.5 | 16.8 | 262 | 2 | US-09-050-739-56 |
| 14 | 140 | 14.1 | 285 | 2 | US-09-095-855-197 |
| 15 | 140 | 14.1 | 285 | 2 | US-09-205-426-197 |
| 16 | 117 | 11.7 | 748 | 1 | US-08-997-080-154 |
| 17 | 117 | 11.7 | 748 | 1 | US-08-997-362-154 |
| 18 | 117 | 11.7 | 748 | 2 | US-09-095-855-154 |
| 19 | 117 | 11.7 | 748 | 2 | US-09-324-542-154 |
| 20 | 117 | 11.7 | 748 | 2 | US-09-205-426-154 |
| 21 | 116 | 11.6 | 167 | 1 | US-08-997-080-112 |
| 22 | 116 | 11.6 | 167 | 1 | US-08-997-362-112 |
| 23 | 116 | 11.6 | 167 | 2 | US-09-095-855-112 |
| 24 | 116 | 11.6 | 167 | 2 | US-09-324-542-112 |
| 25 | 116 | 11.6 | 167 | 2 | US-09-205-426-112 |
| 26 | 114.5 | 11.5 | 28 | 1 | US-08-817-997A-3 |
| 27 | 88 | 8.8 | 1385 | 2 | US-09-252-991A-21919 |

| | | | | | | |
|----|------|-----|------|---|----------------------|--------------------|
| 28 | 87 | 8.7 | 4550 | 1 | US-08-804-227C-8 | Sequence 8, Appli |
| 29 | 87 | 8.7 | 4550 | 1 | US-08-804-198-2 | Sequence 2, Appli |
| 30 | 86 | 8.6 | 357 | 2 | US-09-583-110-3238 | Sequence 3238, Ap |
| 31 | 86 | 8.6 | 370 | 2 | US-09-107-433-3018 | Sequence 3018, Ap |
| 32 | 85.5 | 8.6 | 297 | 2 | US-09-902-540-16434 | Sequence 16434, A |
| 33 | 82.5 | 8.3 | 666 | 1 | US-09-252-991A-17462 | Sequence 17462, A |
| 34 | 81 | 8.1 | 345 | 1 | US-08-282-197C-50 | Sequence 50, Appl |
| 35 | 81 | 8.1 | 592 | 1 | US-08-217-327-8 | Sequence 8, Appli |
| 36 | 79.5 | 8.0 | 200 | 2 | US-09-355-166-18 | Sequence 18, Appl |
| 37 | 78.5 | 7.9 | 309 | 2 | US-09-605-703B-1240 | Sequence 1240, Ap |
| 38 | 78.5 | 7.9 | 309 | 2 | US-09-605-703B-1242 | Sequence 1242, Ap |
| 39 | 78.5 | 7.9 | 1039 | 2 | US-09-409-648-7 | Sequence 7, Appli |
| 40 | 78.5 | 7.9 | 1039 | 2 | US-09-409-648-8 | Sequence 8, Appli |
| 41 | 78.5 | 7.9 | 1039 | 2 | US-09-054-272-10 | Sequence 10, Appl |
| 42 | 78.5 | 7.9 | 1039 | 2 | US-09-949-002-298 | Sequence 298, App |
| 43 | 78.5 | 7.9 | 1039 | 6 | 5196511-2 | Patent No. 5196511 |
| 44 | 78 | 7.8 | 1014 | 2 | US-09-252-991A-17583 | Sequence 17583, A |
| 45 | 77.5 | 7.8 | 495 | 2 | US-09-252-991A-27501 | Sequence 27501, A |

ALIGNMENTS

RESULT 1

US-09-873-075A-1
; Sequence 1, Application US/09873075A
; Patent No. 6960459
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Schroder Glad, Sanne
; APPLICANT: Fukuyama, Shiro
; APPLICANT: Matsui, Tomoko
; TITLE OF INVENTION: Cutinase variants
; FILE REFERENCE: 10038.200-US
; CURRENT APPLICATION NUMBER: US/09/873, 075A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Humicola insolens
US-09-873-075A-1

| | | | | |
|--|-----------------|---|-----------|-------------|
| Query Match | 99.5%; | Score 991; | DB 2; | Length 194; |
| Best Local Similarity | 99.5%; | Pred. No. 6.8e-105; | | |
| Matches 193; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| Qy | 1 | QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIOGVGG | 60 | |
| Db | 1 | QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIOGVGG | 60 | |
| Qy | 61 | PYDAALATNPLPRGTSQANIDEGKRLFALANKKCNTPPVAGGYSQGAALIAAAVSELSC | 120 | |
| Db | 61 | PYDAALATNPLPRGTSQANIDEGKRLFALANKKCNTPPVAGGYSQGAALIAAAVSELSC | 120 | |
| Qy | 121 | AVKSOVGVAFVGYTONLQNEGGTANYPRRTKVCNVDGAVCTGTLIITPAHLSTYIEA | 180 | |
| Db | 121 | AVKSOVGVAFVGYTONLQNEGGTANYPRRTKVCNVDGAVCTGTLIITPAHLSTYIEA | 180 | |
| Qy | 181 | RGEAARFLRDRIRA 194 | | |
| Db | 181 | RGEAARFLRDRIRA 194 | | |
| RESULT 2 | | | | |
| US-08-817-997A-2 | | | | |
| ; Sequence 2, Application US/08817997A | | | | |
| ; Patent No. 5827719 | | | | |
| ; GENERAL INFORMATION: | | | | |
| ; APPLICANT: Sandal, Thomas | | | | |
| ; APPLICANT: Kauppinen, Sakari | | | | |
| ; APPLICANT: Kofod, Lene V. | | | | |

```
; TITLE OF INVENTION: An Enzyme With Lipolytic
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58277190 No. 5827719disk Of No. 5827719th America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,997A
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 7435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4316.204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-817-997A-2

Query Match          99.5%; Score 991; DB 1; Length 229;
Best Local Similarity 99.5%; Pred. No. 8.6e-105;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIQVGG 60
DB 36 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIQVGG 95
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAAVSELG 120
DB 96 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAAVSELG 155
QY 121 AVKEQKGVVALFGYTONLQNRGGIANYPRTKVFNCNVDGAVCTGTLLITPAHLSYTI EA 180
DB 156 AVKEQKGVVALFGYTONLQNRGGIANYPRTKVFNCNVDGAVCTGTLLITPAHLSYTI EA 215
QY 181 RGEAARFLDRIRA 194
DB 216 RGEAARFLDRIRA 229

RESULT 3
US-09-177-234-3
; Sequence 3, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
;
US-09-177-234-8

Query Match          50.2%; Score 499.5; DB 2; Length 232;
Best Local Similarity 50.5%; Pred. No. 1.1e-48;

; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Gliocladium sp.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
;
US-09-177-234-3

Query Match          50.3%; Score 500.5; DB 2; Length 231;
Best Local Similarity 50.0%; Pred. No. 8.8e-49;
Matches 95; Conservative 34; Mismatches 58; Indels 3; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIQVGGPY 62
DB 42 VRDELKRG-GSACPKAILIFARGTMELDNMGLLVGPALAGGLEGLSGNNLWVQVGGQY 100
QY 63 DAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAAVSELGAV 122
DB 101 AANLEGNLFDPGTGPKATQEMLSLLQLADATKCPNSKIVTGGYSQGAALVAAAIKAS 160
QY 123 KEQVKGVALFGYTONLQNRGGIANYPRTKVFNCNVDGAVCTGTLLITPAHLSYTI EA 182
DB 161 RQKIVGTVLFGYTKNKGQVENVSTDLRLVYCNLGDLLICEGTLILVLPPLHLYGVQAAG 220
QY 183 EAARFLDRDI 192
DB 221 PAAQFLASKI 230

RESULT 4
US-09-177-234-8
; Sequence 8, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
;
US-09-177-234-8
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Qy 183 EA 184
Db 245 AA 246

RESULT 8

US-10-114-116-1

; Sequence 1, Application US/10114116

; Patent No. 6828129

; GENERAL INFORMATION:

; APPLICANT: Sumitomo Chemical Co. Ltd.

; TITLE OF INVENTION: Esterase Genes and Use thereof

; FILE REFERENCE: P150409

; CURRENT APPLICATION NUMBER: US/10/114,116

; PRIOR FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: US/09/585,468

; PRIOR FILING DATE: 2000-06-02

; NUMBER OF SEQ ID NOS: 5

; SEQ ID NO 1

; LENGTH: 255

; TYPE: PRT

; ORGANISM: Aspergillus flavus

US-10-114-116-1

Query Match 26.1%; Score 260; DB 2; Length 255;
Best Local Similarity 34.1%; Pred. No. 2.9e-21;
Matches 62; Conservative 30; Mismatches 70; Indels 20; Gaps 6;

Qy 11 SGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHEI--RNWIQGVGPPYDAALAT 68
Db 77 NGFTGACTDYTLVLFARGTSEPGNVGLVGPPLAEAFEGAVGASALSFGQVNG--YSASV-E 134

Qy 69 NFLPRTGSQANIDEGKRLPALANO-----KCPNTPVWAGGYSQGAALIAAAVSELGAV 122
Db 135 GYLGG-----EAGSKAMASQASDILSKCPDTKLVMSGYSGQCGQIVHNAVEQLPAEH 187

Qy 123 KEQVKGVALFGYTONLQNRGGIANYPRETRKVFNCNVGDVACTGTLLITPAHLSTYIEARG 182
Db 188 ASKISSVLLFG---DPYKGLPNVDASRVHTVCHAGDTICENSIVILLPAHLTYAVDVAS 244

Qy 183 EA 184
Db 245 AA 246

RESULT 9

US-10-231-478-1

; Sequence 1, Application US/10231478

; Patent No. 6936445

; GENERAL INFORMATION:

; APPLICANT: KAWABE, TOMOYASU

; APPLICANT: KAWITAMARI, MASASHI

; TITLE OF INVENTION: ENZYME PREPARATION AND METHOD OF USING THE SAME

; FILE REFERENCE: 7372/73243

; CURRENT APPLICATION NUMBER: US/10/231,478

; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: JP 2001-265495

; PRIOR FILING DATE: 2001-09-03

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 255

; TYPE: PRT

; ORGANISM: Aspergillus flavus

US-10-231-478-1

Query Match 26.1%; Score 260; DB 2; Length 255;
Best Local Similarity 34.1%; Pred. No. 2.9e-21;
Matches 62; Conservative 30; Mismatches 70; Indels 20; Gaps 6;

Qy 11 SGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHEI--RNWIQGVGPPYDAALAT 68
Db 77 NGFTGACTDYTLVLFARGTSEPGNVGLVGPPLAEAFEGAVGASALSFGQVNG--YSASV-E 134

Qy 69 NFLPRTGSQANIDEGKRLPALANO-----KCPNTPVWAGGYSQGAALIAAAVSELGAV 122
Db 135 GYLGG-----EAGSKAMASQASDILSKCPDTKLVMSGYSGQCGQIVHNAVEQLPAEH 187
Qy 123 KEQVKGVALFGYTONLQNRGGIANYPRETRKVFNCNVGDVACTGTLLITPAHLSTYIEARG 182
Db 188 ASKISSVLLFG---DPYKGLPNVDASRVHTVCHAGDTICENSIVILLPAHLTYAVDVAS 244
Qy 183 EA 184
Db 245 AA 246

RESULT 10

US-09-050-739-10

; Sequence 10, Application US/09050739

; Patent No. 6641814

; GENERAL INFORMATION:

; APPLICANT: ANDERSEN, Peter

; APPLICANT: NIELSEN, Rikke

; APPLICANT: OETTINGER, Thomas

; APPLICANT: RASMUSSEN, Peter Birk

; APPLICANT: ROSENKRANDS, Ida

; APPLICANT: WELDBINGH, Karin

; APPLICANT: FLORIO, Walter

; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

; FILE REFERENCE: 670001-2002.1

; CURRENT APPLICATION NUMBER: US/09/050,739

; EARLIER FILING DATE: 1998-03-30

; EARLIER APPLICATION NUMBER: 0376/97

; EARLIER FILING DATE: 1997-04-02

; EARLIER APPLICATION NUMBER: 1277/97

; EARLIER FILING DATE: 1997-11-10

; EARLIER APPLICATION NUMBER: 60/044,624

; EARLIER FILING DATE: 1997-04-18

; EARLIER APPLICATION NUMBER: 60/070,488

; EARLIER FILING DATE: 1998-01-05

; NUMBER OF SEQ ID NOS: 173

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 217

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

US-09-050-739-10

Query Match 19.0%; Score 189.5; DB 2; Length 217;
Best Local Similarity 30.8%; Pred. No. 2.6e-13;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

Qy 8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHEIRNIWIQGVGPPYDAALA 67
Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSITGVYA 76

Qy 68 TNFLP-----RGTQANIDEGKRLFALANQKCPNTPWAGGYSQGAALIAAAVSELGAVK 123
Db 77 VNYPASDDYRASANGSGDDSAHIQRTVASCENTRIVLGGYSQGVATVLDLSTSAMPPAVA 136

Qy 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVFNCNVGDVACTGTLLITPAHLS 175
Db 137 DHVAVALFGPSPSGFSMLMGGSLPTIGPLYSSKTNLNCAPDDPCTCTGGGNIM-AHVS 195

Qy 176 YTIEA-RGEARFLRDRI 192

Db 196 YVQSGMTSQAATFAANRL 213

RESULT 11

US-09-050-739-14

; Sequence 14, Application US/09050739

; Patent No. 6641814

; GENERAL INFORMATION:

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; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLING, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-09-050-739-14

Query Match      18.9%; Score 188.5; DB 2; Length 219;
Best Local Similarity 31.7%; Pred. No. 3.4e-13;
Matches 66; Conservative 32; Mismatches 75; Indels 35; Gaps 11;

Qy      8 GLEGSANACPDALLIFARGSTEPNNWGITVGPALANGLESHI-RNIWIQVGGPYDAAL 66
Db      25 GAVAPATAACPDAEWVFARGFEPPGIG-ITVGNAFVSAIRSKVNKNGVYAVKYPAD--- 80

Qy      67 ATNPLPRTSQANTDEGKRIFALANQKCPNTPVAVGYSQCAA---LFAAAVSELSGAVK 123
Db      81 --NOIDVGAN-----DMSAHQSMAN-SCPNTRLVPGGYSGLGAATVDVVLAVPTQMWGFTN 133

Qy      124 -----EQVKVALFGYQTQNLQRGGIANYP---RERTKFCVKNVGDAVCTGTLLIT--- 170
Db      134 PLPPGSDHIAAVALFG--NGSQWVGPIITNFPSPAYNDRITIELCHGDDPVCVHPADPNTWEA 191

Qy      171 --PAHLSYTIIEARG---EAPRFLRDRIR 193
Db      192 NWPOHLAGAYVSSGMVWNAQADFVAGKLQ 219

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RESULT 12
US-09-050-739-52
; Sequence 52, Application US/09050739
; Patent No. 6641814
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OTTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488

```

; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-52

Query Match 17.9%; Score 178; DB 2; Length 226;
Best Local Similarity 33.2%; Pred.No 5.6e-12;
Matches 64; Conservative 24; Mismatches 75; Indels 30; Gaps 11;

Qy 17 CPDAILFARGSTEPGNMGITVGPALLANGLESII-RNIWITQGVGGPYDAALATNFIPLRGT 75
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 47 CPDAEVVFARGTGEPCLG-RVGAQFVSSLRQQTNSIGTYGVNYPANG----DFAAAD 101
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 76 SQANIDBGRKFLPALANQKCPNTPVVAGVYSQGA---LIAAA-----VSELSGAVKEQ 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 102 GANDASDHIIQOMASA---CRATRLVLGGYSQGAVIDIVTAAPLGLGFTQPLPPAADH 158
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 126 VKGVALFGYTONLQNRGG---IANYPR--ERTKVFNCVGDVACT-GTLIITPAHLSYITIE 179
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 IAAIALFG---NPSGRAGGLMSALTQFGSKTILNCNGDPICSDGNR--WRAHLGYVPG 213
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 180 ARGEAARFLRDRI 192
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 MTNQARFVASRI 226
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-050-739-56
; Sequence 56, Application US/09050739
; Patent No. 6641814
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-56

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| Query Match | 16.8%; | Score 167.5; | DB 2; | Length 262; |
| Best Local Similarity | 31.8%; | Pred. No. 1.1e-10; | | |
| Matches | 67; | Conservative 22; | Mismatches 69; | Indels 53; Gaps 12; |
| Qy | 14 | ANACPDALLIFRGSTEGNMGITVCPALANGLESIRNIWIOGVG-- | GPYDAALATNF | 70 |
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| Db | 41 | ADGCPDAEVTFKGTGEPGIG-RVQAFVDSLR----- | QQTGMEIGVTFPVNVAASR | 91 |
| | | : : : : | | |
| Qy | 71 | LP-RGTSGQANIDEGKRLFALANQKCPNTFVAGVSGQAAL-- | IAAAV-----SEPS | 119 |
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Db 92 LQHGDDGAN-DAISHIKSMAS-SCNTKVLGGYSQGATVIDIAGVPLGSGISFGSPLP 149
QY 120 GAVKEQVKGVALFGYTONLQNRGG-----IANYPRERTKVFNCVGVDAVCTGTILITPAHL 174
Db 150 AAYADNVAAVVFG---NFSNRAGGSSLSPLFGSKAIDLCLNPTDPICTIC-----HV 197
QY 175 SVTIRARG-----EAAFLRDRIRA 194
Db 198 GPGNEFSGHIDGYIPTTYTTOAASFVQRLRA 228

RESULT 14

US-09-095-855-197
; Sequence 197, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITL OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/705,347
; APPLICATION NUMBER: 29-AUG-1996
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-095-855-197

Query Match 14.1%; Score 140; DB 2; Length 285;
Best Local Similarity 29.2%; Pred. No. 1.7e-07;
Matches 62; Conservative 30; Mismatches 68; Indels 52; Gaps 15;
QY 9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWQGVGYPYDAALA 67
Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVGE---QSVG-----TYA 76
QY 68 TNF-----LPRGTSQANIDEGKRLFALANOKCPTNPVWAGYSQGAALIAAAV--- 115

Db 77 VNYPAGEFDKSAAPMGAAADAS---GRVQWADN---CPDTKVLVGGMSQAGVIDLITVDP 131
QY 116 -----SELSGAVKEQVKGVALFGYTONLQNRGG-----IANYPRERTKVFNCVGVDA 161
Db 132 RPLGRFTPTMPPRVADHVAAVVFG--NPLRDIRGGGGLPQMSTGYGPKSIDLCALDDP 189
QY 162 VCTGTLLITPAHLSYT-----IEARGEAAFLR 189
Db 190 FCSPGFNL-PAHFAYADNGMVE---EAAAFAR 217

RESULT 15

US-09-205-426-197
; Sequence 197, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITL OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 197
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-197

Query Match 14.1%; Score 140; DB 2; Length 285;
Best Local Similarity 29.2%; Pred. No. 1.7e-07;
Matches 62; Conservative 30; Mismatches 68; Indels 52; Gaps 15;
QY 9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWQGVGYPYDAALA 67
Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVGE---QSVG-----TYA 76
QY 68 TNF-----LPRGTSQANIDEGKRLFALANOKCPTNPVWAGYSQGAALIAAAV--- 115
Db 77 VNYPAGEFDKSAAPMGAAADAS---GRVQWADN---CPDTKVLVGGMSQAGVIDLITVDP 131
QY 116 -----SELSGAVKEQVKGVALFGYTONLQNRGG-----IANYPRERTKVFNCVGVDA 161
Db 132 RPLGRFTPTMPPRVADHVAAVVFG--NPLRDIRGGGGLPQMSTGYGPKSIDLCALDDP 189
QY 162 VCTGTLLITPAHLSYT-----IEARGEAAFLR 189
Db 190 FCSPGFNL-PAHFAYADNGMVE---EAAAFAR 217

Search completed: February 4, 2006, 04:57:52
Job time : 49 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 05:08:15 ; Search time 177 Seconds
(without alignments)
457.960 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996
Sequence: 1 QLGAIENGLESGSANACPD.....SYTIEARGEARFLDRIRA 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 991 | 99.5 | 194 | 3 | US-09-873-075A-1 |
| 2 | 991 | 99.5 | 194 | 4 | US-10-152-300-1 |
| 3 | 991 | 99.5 | 194 | 5 | US-10-846-123-1 |
| 4 | 542.5 | 54.5 | 199 | 4 | US-10-152-300-2 |
| 5 | 542.5 | 54.5 | 199 | 5 | US-10-846-123-2 |
| 6 | 268.5 | 27.0 | 245 | 4 | US-10-424-599-175880 |
| 7 | 260 | 26.1 | 255 | 4 | US-10-114-116-1 |
| 8 | 260 | 26.1 | 255 | 4 | US-10-114-115A-1 |
| 9 | 260 | 26.1 | 255 | 4 | US-10-231-478-1 |
| 10 | 209.5 | 21.0 | 236 | 4 | US-10-425-115-327696 |
| 11 | 206 | 20.7 | 154 | 4 | US-10-425-115-247113 |
| 12 | 189.5 | 19.0 | 217 | 3 | US-09-791-171-10 |
| 13 | 189.5 | 19.0 | 217 | 3 | US-09-804-980-10 |
| 14 | 189.5 | 19.0 | 217 | 3 | US-09-855-604-259 |
| 15 | 189.5 | 19.0 | 217 | 3 | US-09-855-604-259 |
| 16 | 189.5 | 19.0 | 217 | 4 | US-10-138-473-10 |
| 17 | 189.5 | 19.0 | 217 | 4 | US-10-620-246-10 |
| 18 | 189.5 | 19.0 | 238 | 3 | US-09-855-604-261 |
| 19 | 189.5 | 19.0 | 238 | 3 | US-09-855-604-261 |
| 20 | 188.5 | 18.9 | 219 | 3 | US-09-791-171-14 |
| 21 | 188.5 | 18.9 | 219 | 3 | US-09-804-980-14 |
| 22 | 188.5 | 18.9 | 219 | 4 | US-10-620-246-14 |
| 23 | 178 | 17.9 | 226 | 3 | US-09-791-171-52 |
| 24 | 178 | 17.9 | 226 | 3 | US-09-804-980-52 |
| 25 | 178 | 17.9 | 226 | 4 | US-10-620-246-52 |
| 26 | 167.5 | 16.8 | 262 | 3 | US-09-791-171-56 |
| 27 | 167.5 | 16.8 | 262 | 3 | US-09-804-980-56 |

| | | | | | | |
|----|-------|------|------|---|----------------------|-------------------|
| 28 | 167.5 | 16.8 | 262 | 4 | US-10-138-473-56 | Sequence 56, Appl |
| 29 | 167.5 | 16.8 | 262 | 4 | US-10-620-246-56 | Sequence 56, Appl |
| 30 | 140 | 14.1 | 285 | 4 | US-10-051-643-197 | Sequence 197, App |
| 31 | 140 | 14.1 | 285 | 4 | US-10-205-979-34 | Sequence 34, Appl |
| 32 | 124 | 12.4 | 248 | 4 | US-10-425-115-288506 | Sequence 288506, |
| 33 | 120.5 | 12.1 | 233 | 4 | US-10-425-115-194225 | Sequence 194225, |
| 34 | 117 | 11.7 | 748 | 3 | US-09-880-505-154 | Sequence 154, App |
| 35 | 117 | 11.7 | 748 | 4 | US-10-051-643-154 | Sequence 154, App |
| 36 | 116 | 11.6 | 167 | 3 | US-09-880-505-112 | Sequence 112, App |
| 37 | 116 | 11.6 | 167 | 4 | US-10-051-643-112 | Sequence 112, App |
| 38 | 106 | 10.6 | 205 | 4 | US-10-425-115-335015 | Sequence 335015, |
| 39 | 96 | 9.6 | 336 | 4 | US-10-080-170-627 | Sequence 627, App |
| 40 | 96 | 9.6 | 336 | 4 | US-10-080-170-627 | Sequence 627, App |
| 41 | 96 | 9.6 | 336 | 4 | US-10-468-356-627 | Sequence 627, App |
| 42 | 88 | 8.8 | 1356 | 4 | US-10-077-111-10 | Sequence 10, Appl |
| 43 | 87 | 8.7 | 336 | 4 | US-10-080-170-25 | Sequence 25, Appl |
| 44 | 87 | 8.7 | 336 | 4 | US-10-080-170-25 | Sequence 25, Appl |
| 45 | 87 | 8.7 | 336 | 4 | US-10-468-356-25 | Sequence 25, Appl |

ALIGNMENTS

RESULT 1
US-09-873-075A-1
; Sequence 1, Application US/09873075A
; Patent No. US20020123123A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Schroder Glad, Sanne
; APPLICANT: Fukuyama, Shiro
; APPLICANT: Matsui, Tomoko
; TITLE OF INVENTION: Cutinase variants
; FILE REFERENCE: 10038.200-US
; CURRENT APPLICATION NUMBER: US/09/873,075A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Humicola insolens
; US-09-873-075A-1

| | | | | |
|---------------------------------------|-----------------|--|-----------|-------------|
| Query Match | 99.5% | Score 991; | DB 3; | Length 194; |
| Best Local Similarity | 99.5% | Pred. No. 8.8e-95; | | |
| Matches 193; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| Qy | 1 | QLGAIENGLESGSANACPDAILIFARGSTFPGNMGITVGPALANGLESHERNIWIQVGG | 60 | |
| Db | 1 | QLGAIENGLESGSANACPDAILIFARGSTFPGNMGITVGPALANGLESHERNIWIQVGG | 60 | |
| Qy | 61 | PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSELSS | 120 | |
| Db | 61 | PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSELSS | 120 | |
| Qy | 121 | AVKEQVKGVALFGYTONLQNRGGTANYPRRTKVPFCNVGDVCTGTLITTPAHLSTTIERA | 180 | |
| Db | 121 | AVKEQVKGVALFGYTONLQNRGGTANYPRRTKVPFCNVGDVCTGTLITTPAHLSTTIERA | 180 | |
| Qy | 181 | RGEARFLDRIRA 194 | | |
| Db | 181 | RGEARFLDRIRA 194 | | |
| RESULT 2 | | | | |
| US-10-152-300-1 | | | | |
| ; Sequence 1, Application US/10152300 | | | | |
| ; Publication No. US20030051836A1 | | | | |
| ; GENERAL INFORMATION: | | | | |
| ; APPLICANT: Borch, Kim | | | | |
| ; APPLICANT: Lund, Henrik | | | | |
| ; APPLICANT: Sharyo, Masaki | | | | |


```
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/152,300
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Humicola insolens
US-10-152-300-1

Query Match          99.5%; Score 991; DB 4; Length 194;
Best Local Similarity 99.5%; Pred. No. 8.8e-95;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60
Db      1  QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60

QY      61  PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGYSQGAALIAAAVSELG 120
Db      61  PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGYSQGAALIAAAVSELG 120

QY      121  AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVCNVDGAVCTGTLLITPAHLSYTTIEA 180
Db      121  AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVCNVDGAVCTGTLLITPAHLSYTTIEA 180

QY      181  RGEAARFLDRIRA 194
Db      181  RGEAARFLDRIRA 194

RESULT 3
US-10-846-123-1
; Sequence 1, Application US/10846123
; Publication No. US20040226672A1
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/846,123
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Humicola insolens
US-10-846-123-1

Query Match          99.5%; Score 991; DB 5; Length 194;
Best Local Similarity 99.5%; Pred. No. 8.8e-95;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60
Db      1  QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60

QY      61  PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGYSQGAALIAAAVSELG 120
Db      61  PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGYSQGAALIAAAVSELG 120
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QY      121  AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVCNVDGAVCTGTLLITPAHLSYTTIEA 180
Db      121  AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVCNVDGAVCTGTLLITPAHLSYTTIEA 180

QY      181  RGEAARFLDRIRA 194
Db      181  RGEAARFLDRIRA 194

RESULT 4
US-10-152-300-2
; Sequence 2, Application US/10152300
; Publication No. US20030051836A1
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/152,300
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Fusarium solani pisi
US-10-152-300-2

Query Match          54.5%; Score 542.5; DB 4; Length 199;
Best Local Similarity 55.9%; Pred. No. 4.9e-48;
Matches 105; Conservative 31; Mismatches 49; Indels 3; Gaps 2;

QY      9  LEGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGGPYDAAL 66
Db      8  LINGSASCADVIPIYARGSTETGNLG-TLGFSTASNLSEAFGKDGWVIQGVGGAYRATL 66

QY      67  ATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGYSQGAALIAAAVSELGAVKEQV 126
Db      67  GDNALPRGTSSAATREMLGLFQQANTKCPDYLATAGYSQGAALAAASIEDLDSAIRDKI 126

QY      127  KGVALFGYTONLQNRGGIANYPRERTKVCNVDGAVCTGTLLITPAHLSYTTIEARGEAA 186
Db      127  AGTVLFGYTKNLQNRGRIPNYPADRTKVPCTGDLVCTGSLIVAAPHLAYGPDARGPAPE 186

QY      187  FLDRIRA 194
Db      187  FLIEKVRA 194

RESULT 5
US-10-846-123-2
; Sequence 2, Application US/10846123
; Publication No. US20040226672A1
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/846,123
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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      188 ASKISSVLLFG---DPYKKGALPNVDASRVHVTCHAGPTICENSVIILLPAHLTYYADVNAS 244
      183 EA 184
      245 AA 246

      RESULT 9
      US-10-231-478-1
      ; Sequence 1, Application US/10231478
      ; Publication No. US20030124683A1
      ; GENERAL INFORMATION:
      ; APPLICANT: KAWABE, TOMOYASU
      ; APPLICANT: KAMITAMARI, MASASHI
      ; TITLE OF INVENTION: ENZYME PREPARATION AND METHOD OF USING THE SAME
      ; FILE REFERENCE: 7372/73243
      ; CURRENT APPLICATION NUMBER: US/10/231.478
      ; CURRENT FILING DATE: 2002-12-09
      ; PRIOR APPLICATION NUMBER: JP 2001-265495
      ; PRIOR FILING DATE: 2001-09-03
      ; NUMBER OF SEQ ID NOS: 2
      ; SOFTWARE: PatentIn Ver. 2.1
      ; SEQ ID NO 1
      ; LENGTH: 255
      ; TYPE: PR1
      ; ORGANISM: Aspergillus flavus
      US-10-231-478-1

```

| | | | | | | | |
|-----------------------|--------|--|----------|------------|-----|--------|----------|
| Query Match | 26.1%; | Score | 260; | DB | 4; | Length | 255; |
| Best Local Similarity | 34.1%; | Pred. No. | 1.8e-18; | | | | |
| Matches | 62; | Conservative | 30; | Mismatches | 70; | Indels | 20; Gaps |
| | | | | | | | 6; |
| QY | 11 | SGSANACPDAILFARGSTPGNMGITVGPALANGLESHT--RNIIQTGGVGYPDAALAT | 68 | | | | |
| Db | 77 | NGFTGACTDVTLVFARGTSEPGNVGLVGPPLAEAFEGAVGASALSFGVNG-YSA ^{SV-E} | 134 | : | : | : | : |
| QY | 69 | NFLPRGTSQANI ^{DEG} KRLFPALNQ-----KCPNTFVVAGGYSGCALIAAAYSEL ^S GV | 122 | : | : | : | : |
| Db | 135 | GYL ^{AGG} -----EAAGSKAMASQASDILSKCPDTKLVMGSYGQQCQIVHNAVEQLPAEH | 187 | : | : | : | : |
| QY | 123 | KEOVKGVALFGYTQNLRNGGIANYPRRTKVFCNVGD ^A VCTGLTIITPAHLSYTTIEAR ^G | 182 | : | : | : | : |
| Db | 188 | ASKISSVLLE ^G ---DPYK ^G KALPNVDASRVHTVCHAGDTTCENSVIILPAHLTVADV ^S | 244 | : | : | : | : |
| QY | 183 | EA | 184 | | | | |
| Db | 245 | AA | 246 | | | | |

```

RESULT 10
US-10-425-115-327696
; Sequence 327696, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 327696
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(236)
; OTHER INFORMATION: unsure at all Xaa locations

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; FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_61927C.1.pep
US-10-425-115-327696

Query Match      21.0%; Score 209.5; DB 4; Length 236;
Best Local Similarity 32.1%; Pred. No. 3e-13;
Matches 63; Conservative 30; Mismatches 78; Indels 25; Gaps 8;

Qy      7 NGLSEGSANACPDAILIFARGSTEPGNWG--ITVGPALANGLESHI---RNIIWIGVGGP 61
Db      56 NQUTDGT--ACRPISVIYAGTSGAGNVGSASVGPLFFNQIASRVGGETSOLAQGTYP 113
Qy      62 YDAALATNFIPLRG-----TSQANIDEKRLIFALANQKCPNTPPVAGGYSQGAALIAAAS 116
Db      114 ---ASVSGFLAGGDAAGSTMTN-----LISSTATCPNTKIVLAGYSQGAQLVHNAAG 164
Qy      117 ELSGAVKEQKVALFGYTONLQNRGGIANYPRRTKVCNVGDAVCTGTLIIIPAHLSY 176
Db      165 RTTANAAKVAAVVVFGDPRKGOSLSPIA---ASKVLTICHGDGNICEGSSITIAHLT 221
Qy      177 TIEARGEAAARFLRDRI 192
Db      222 QMDV-ATAKAFVAGKV 236

RESULT 11
US-10-425-115-247113
; Sequence 247113, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;   APPLICANT: La Rosa, Thomas J.
;   APPLICANT: Kovalic, David K.
;   APPLICANT: Zhou, Yihua
;   APPLICANT: Cao, Yongwei
;   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;   TITLE OF INVENTION: Plants
;   FILE REFERENCE: 38-21(53222)B
;   CURRENT APPLICATION NUMBER: US/10/425,115
;   CURRENT FILING DATE: 2003-04-28
;   NUMBER OF SEQ ID NOS: 369326
;   SEQ ID NO 247113
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_156956C.1.pep
US-10-425-115-247113

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```

Query Match      20.7%; Score 206; DB 4; Length 154;
Best Local Similarity 34.6%; Pred. No. 4e-13;
Matches 56; Conservative 24; Mismatches 72; Indels 10; Gaps 6;

Qy      34  MGIIVCPALANGLESHI--RNIIQGVGGPYDAALATNFI PRGTSQANIDEGKRLFALAN 91
Db      1  VGTVAGPPFFKAI GEKIQDQKLVAGV--DYSASIA-GIMQMG-DKAGSEKMSLVTVEAV 56

Qy      92  QKCPNTPVWAGGYSGQAALIAAAVSELSGAVKEQVGVALFGYITQNLQNRGGIANYPR 151
Db      57  KCKPCKTIVMSGYSQGNMLVHNAARALPAETTTAKVAAVLNFG---DPFQFQAIGQVPADR 113

Qy      152  TKVFCNVGDVACTGTTLITPAHLSYTIARGEAAARFLDRIR 193
Db      114  VKIICHAGDGVCGAGTAAITPDHLTYSKDA-GAAADFVASKVQ 154

RESULT 12
US-09-791-171-10
; Sequence 10, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas

```

```
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-10

Query Match      19.0%; Score 189.5; DB 3; Length 217;
Best Local Similarity 30.8%; Pred. No. 3.3e-11;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

QY 8 GLESGANACPDAILIFARGSTPEGNMGTIVGPALANGLESHIRNIWIOGVGGPYDAALA 67
Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSIGVYA 76
QY 68 TNFLP-----RGTSQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELSGAVK 123
Db 77 VNYPASDDYRASNGSDDASAHQRTVASCNTRIVLGYSQSGATVIDLSTSAMPPAVA 136
QY 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVFNCVGDVAVCTGTLLITPAHLS 175
Db 137 DHVAALVAFGEPSGSSGFWMLWGGSLPTIGPLYSSKTNLCAPDDPCTCTGGNIN-AHVS 195
QY 176 YTIEA-RGEAARFLRDRI 192
Db 196 YVQSGMTSQAATFAANRL 213
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-10

Query Match      19.0%; Score 189.5; DB 3; Length 217;
Best Local Similarity 30.8%; Pred. No. 3.3e-11;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

QY 8 GLESGANACPDAILIFARGSTPEGNMGTIVGPALANGLESHIRNIWIOGVGGPYDAALA 67
Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSIGVYA 76
QY 68 TNFLP-----RGTSQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELSGAVK 123
Db 77 VNYPASDDYRASNGSDDASAHQRTVASCNTRIVLGYSQSGATVIDLSTSAMPPAVA 136
QY 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVFNCVGDVAVCTGTLLITPAHLS 175
Db 137 DHVAALVAFGEPSGSSGFWMLWGGSLPTIGPLYSSKTNLCAPDDPCTCTGGNIN-AHVS 195
QY 176 YTIEA-RGEAARFLRDRI 192
Db 196 YVQSGMTSQAATFAANRL 213
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-10

Query Match      19.0%; Score 189.5; DB 3; Length 217;
Best Local Similarity 30.8%; Pred. No. 3.3e-11;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

QY 8 GLESGANACPDAILIFARGSTPEGNMGTIVGPALANGLESHIRNIWIOGVGGPYDAALA 67
Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSIGVYA 76
QY 68 TNFLP-----RGTSQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELSGAVK 123
Db 77 VNYPASDDYRASNGSDDASAHQRTVASCNTRIVLGYSQSGATVIDLSTSAMPPAVA 136
QY 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVFNCVGDVAVCTGTLLITPAHLS 175
Db 137 DHVAALVAFGEPSGSSGFWMLWGGSLPTIGPLYSSKTNLCAPDDPCTCTGGNIN-AHVS 195
QY 176 YTIEA-RGEAARFLRDRI 192
Db 196 YVQSGMTSQAATFAANRL 213
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-10
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Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSIGVYA 76
QY 68 TNFLP-----RGTSQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELSGAVK 123
Db 77 VNYPASDDYRASNGSDDASAHQRTVASCNTRIVLGYSQSGATVIDLSTSAMPPAVA 136
QY 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVFNCVGDVAVCTGTLLITPAHLS 175
Db 137 DHVAALVAFGEPSGSSGFWMLWGGSLPTIGPLYSSKTNLCAPDDPCTCTGGNIN-AHVS 195
QY 176 YTIEA-RGEAARFLRDRI 192
Db 196 YVQSGMTSQAATFAANRL 213

RESULT 14
US-09-855-604-259
; Sequence 259, Application US/09855604
; Publication No. US20040214165A1
; GENERAL INFORMATION:
; APPLICANT: GICOUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: GOGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 259
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604-259

Query Match      19.0%; Score 189.5; DB 3; Length 217;
Best Local Similarity 30.8%; Pred. No. 3.3e-11;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

QY 8 GLESGANACPDAILIFARGSTPEGNMGTIVGPALANGLESHIRNIWIOGVGGPYDAALA 67
Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSIGVYA 76
QY 68 TNFLP-----RGTSQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELSGAVK 123
Db 77 VNYPASDDYRASNGSDDASAHQRTVASCNTRIVLGYSQSGATVIDLSTSAMPPAVA 136
QY 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVFNCVGDVAVCTGTLLITPAHLS 175
Db 137 DHVAALVAFGEPSGSSGFWMLWGGSLPTIGPLYSSKTNLCAPDDPCTCTGGNIN-AHVS 195
QY 176 YTIEA-RGEAARFLRDRI 192
Db 196 YVQSGMTSQAATFAANRL 213

RESULT 15
US-09-855-604-259
; Sequence 259, Application US/09855604
; Publication No. US20050158714A9
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; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: COGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 259
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604-259
```

```
Query Match          19.0%; Score 189.5; DB 3; Length 217;
Best Local Similarity 30.8%; Pred.No. 3.3e-11;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

QY      8 GLESGSANCPDAILIFARGSTPEGNNGITVGPALANGLESHIRNIWIQVGGPYDAALA 67
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
26 GGRAHADPCSDIADVAFKTHQASGLG-DVGEAFVDSLTSQ-----VGGRSIGVYA 76
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      68 TNFLP-----RGTSQANIDEGKRLFALANQKPNTPVVAGYSQGAALIAAAVSELSGAVK 123
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
77 VNVPSDDYRASASNGSDDASAHIQRTVASCPTNTRIVLGGYSQGATVIDLSTAMPPIVA 136
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      124 EQYKGVALF-----GYTONLQNRGG---IANYPRETKVFCNVGDVCTGLTIITPAHLS 175
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
137 DHVAVALFGEPSGSSGSSMLWGGSLFTTIGPLYSSKTNILCAPDDPCTCTGGNIM-AHVS 195
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      176 YTIEA-RGEAARELRDRI 192
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 YVQSGMTSQAATPANRL 213
```

Search completed: February 4, 2006, 05:11:43
Job time : 178 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2006, 05:08:55 ; Search time 15 Seconds
(without alignments)
151.554 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGATENGLESGSANACPD.....SYTIARGENARFLRDIRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New.*

1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 189.5 | 19.0 | 217 | 7 | US-11-052-554A-331 |
| 2 | 82.5 | 8.3 | 138 | 6 | US-10-467-657-2928 |
| 3 | 79.5 | 8.0 | 200 | 7 | US-11-179-977-18 |
| 4 | 79 | 7.9 | 630 | 6 | US-10-517-939-42 |
| 5 | 77 | 7.7 | 575 | 7 | US-11-185-342-3 |
| 6 | 76.5 | 7.7 | 436 | 6 | US-10-467-657-7578 |
| 7 | 76.5 | 7.7 | 7968 | 7 | US-11-143-980-49 |
| 8 | 76 | 7.6 | 710 | 7 | US-11-143-980-40 |
| 9 | 75.5 | 7.6 | 1889 | 7 | US-11-102-476-46 |
| 10 | 75 | 7.5 | 481 | 6 | US-10-467-657-4396 |
| 11 | 75 | 7.5 | 575 | 7 | US-11-185-342-19 |
| 12 | 75 | 7.5 | 575 | 7 | US-11-185-342-21 |
| 13 | 74.5 | 7.5 | 463 | 6 | US-10-531-844-2 |
| 14 | 74 | 7.4 | 424 | 7 | US-11-138-642-13 |
| 15 | 74 | 7.4 | 424 | 7 | US-11-047-383-10 |
| 16 | 74 | 7.4 | 424 | 7 | US-11-138-882-13 |
| 17 | 73.5 | 7.4 | 506 | 6 | US-10-641-678-69 |
| 18 | 73 | 7.3 | 1013 | 7 | US-11-103-957-9 |
| 19 | 73 | 7.3 | 1531 | 7 | US-11-103-957-15 |
| 20 | 72.5 | 7.3 | 592 | 6 | US-10-467-657-550 |
| 21 | 72 | 7.2 | 1571 | 7 | US-11-052-554A-2 |
| 22 | 71.5 | 7.2 | 1438 | 6 | US-10-453-372-796 |
| 23 | 71 | 7.1 | 463 | 7 | US-11-052-554A-261 |
| 24 | 70.5 | 7.1 | 250 | 7 | US-11-054-515-73 |
| 25 | 70.5 | 7.1 | 1225 | 6 | US-10-453-372-798 |

ALIGNMENTS

RESULT 1

US-11-052-554A-331

; Sequence 331, Application US/11052554A

; Publication No. US20050288866A1

; GENERAL INFORMATION:

; APPLICANT: Sachdeva, et al.

; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

; FILE REFERENCE: 30853/40359A

; CURRENT APPLICATION NUMBER: US/11/052,554A

; CURRENT FILING DATE: 2005-02-07

; PRIOR APPLICATION NUMBER: US 60/589,227

; PRIOR FILING DATE: 2004-07-20

; PRIOR APPLICATION NUMBER: IN 173/DEL/2004

; PRIOR FILING DATE: 2004-02-06

; NUMBER OF SEQ ID NOS: 763

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 331

; LENGTH: 217

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis H37Rv

US-11-052-554A-331

Query Match 19.0%; Score 189.5; DB 7; Length 217;

Best Local Similarity 30.8%; Pred. No. 3.4e-11;

Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

Qy 8 GLESGSANACPDAILIPARGSTPEGNMGIIVGPALANGLESHIRNIWIQVGGPYDAALA 67

Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSGTGVYA 76

Qy 68 TNELP---RGTQANTIDEGKRLPALANQKCPNTPVAGGYSQGAALIAAAVSELSGAVK 123

Db 77 VNYPSADYRASANGSDASAHITQRTVASCPNTRIVLGGYSQGAIVDLSTAMPYVA 136

Qy 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVFNCVNGDAVCTGTTLITPAHLS 175

Db 137 DHVAVALFGPSSGFSMLWGGGSLPTIGLYSSKTNILCAPDDPCTCTGGNIM-AHVS 195

Qy 176 YTI EA-RGEAARFLRDRI 192

Db 196 YVQSGMTSQAATFAANRL 213

RESULT 2

US-10-467-657-2928

; Sequence 2928, Application US/10467657

; Publication No. US20050260581A1

```

; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2928
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2928

Query Match      8.3%; Score 82.5; DB 6; Length 138;
Best Local Similarity 29.8%; Pred. No. 0.33;
Matches 36; Conservative 18; Mismatches 18; Indels 31; Gaps 8;

QY 27 GSTEPCGNGITVG-----PA-LANGLESHIRNIWQGV-----GGPYDAALATNPLP 72
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 19 GCSKGNAGFLVGGQILVASGQPAEIEGCIQRLNILLQVFMVQDEPYIA--VTCFL- 75
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 73 RGTSONIDEGKRLFALANQKCNTPVAVGGYSGQAALIAAANVSELGAVKEQVGVLP 132
   :::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 76 --QTASGVQVGLRL-----DVECPHFPVACGLCEKGVSWA-----GGAVOR----IAAF 121
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 133 G 133
Db 122 G 122

RESULT 3
US-11-179-977-18
; Sequence 18, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-18

Query Match      8.0%; Score 79.5; DB 7; Length 200;
Best Local Similarity 22.9%; Pred. No. 1;
Matches 47; Conservative 20; Mismatches 63; Indels 75; Gaps 9;

QY 3 GAJENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGPPY 62
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 21 GGNHDLISLGRFDPAHLLVGRS-----VLEGNMPRFKRL-SEGVDK 67
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 63 DAALAT-----NPLRGTSQANIDEGKRLFALANQKCNTPVAVGGYSGQAALIAAANVSEL 118
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 68 DLVVRTRELKDFIDEAAETHQFNRR-----VIAVGSNGANIAAS----- 108
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 119 SGAVKEQVGVLPFGYTQNLQNRGGIANYPRRTK-----VFCNVG--DAVCTG 165
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 109 -----LLFHYKDVLL--KGAILHHPVMPVIRGIELPDMAGLPVFIGAGKYDPLCTK 155
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 166 TLIIITPAHLSYTTAEARCEAREFLRD 190
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```

Db 156 -----EESBELRYLRD 167

RESULT 4
US-10-517-939-42
; Sequence 42, Application US/10517939
; Publication No. US2006000343A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(37)
US-10-517-939-42

Query Match      7.9%; Score 79; DB 6; Length 630;
Best Local Similarity 24.3%; Pred. No. 5.2;
Matches 42; Conservative 19; Mismatches 70; Indels 42; Gaps 8;

QY 15 NACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGPPY-DAAL----- 66
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 408 NNIPVKARTTFVWGAQSPALNNLSGPEVAVEIEQ-----WIRDYCTRYPTDAMIDVNEA 462
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 67 ATNPLRGTSQANIDEG--KLEFALANQKCNTPVAVGY-----SOGAA 109
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 463 VPGHOPAGYARAFGNWNIQVFLARQYCPNSILILNDYNNIRWQHNEFIALAKAQNY 522
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 110 LIAAAVS--ELSGAVKEQVGVLPFGYTQNLQNRGGIANYPRRTKVFNCVNG 160
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 523 IDAVGLQAHKLGMTAAQVKT-----IDNIWNVQVKPIYISE-----YDIGD 565
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 5
US-11-185-342-3
; Sequence 3, Application US/11185342
; Publication No. US20060021093A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Philip E.
; APPLICANT: Hinson, Todd K.
; APPLICANT: Carr, Brian
; APPLICANT: Duck, Nicholas B.
; TITLE OF INVENTION: GDC-1 GENES CONFERRING HERBICIDE
; FILE REFERENCE: 045600/275114
; CURRENT APPLICATION NUMBER: US/11/185,342
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: US/10/796,953
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: 60/453,237
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 21
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Db 184 GADPSG-QGDSQAFDAIAA-AQGGVWIPPGDYRLT---SSLING-----VQNVTLQAG 234
QY 60 GPYDAALATNPLPRGTSQANID-EGKRLPALANQKCPNTP--VVAGGYSGQAALIAAAYS 116
Db 235 SMHSVHTSRFDIQSSSSGVHVKDFAVIGEVTERVDSNPDNPFVNGSLGPG-----S 286
QY 117 ELSGAVKEQVK-GVALFGYTONI-----QNRGGIANYPRRTKVFNCVGD 160
Db 287 SVSGMWLOHLKVLGWLGMGNNDNLVVENRFLDMTADGLNLNGSAKVRVRNFRNQGD 345

RESULT 9

US-11-102-476-46
; Sequence 46, Application US/11102476
; Publication No. US20050271680A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Pu
; APPLICANT: Palaniappan, Raghavan U.M.
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Novel Immunogenic Proteins of Leptospira
; FILE REFERENCE: 1153.080US1
; CURRENT APPLICATION NUMBER: US/11/102,476
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: PCT/US2003/32385
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/417721
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 1889
; TYPE: PRT
; ORGANISM: Leptospira interrogans
US-11-102-476-46

Query Match 7.6%; Score 75.5; DB 7; Length 1889;
Best Local Similarity 19.1%; Pred. No. 47;
Matches 49; Conservative 35; Mismatches 73; Indels 99; Gaps 9;
QY 8 GLESGSANACPDAILIFARGSTPEGNGITVGPALANGLESHIRNIWQVGGPYDAALA 67
Db 110 GITSGSS-----IIKAYNGLYSEQKITVTFAILNSIQV-----TSLE 147
QY 68 TNPLPRGTSQANIDEGKRLPAL-----ANQKCPNTPV-----AGGY 104
Db 148 SGLTPKGTN-----RLSAIGFSDGSHQDISNDPLIYWSSNPDLVQVDDSLASGI 200
QY 105 SOGAALIAAASVLSGAVKEQVKGVALFGYVQ-----136
Db 201 NLGTAHIRASFQSKQGA-BEMTVGDAVLSQIQVTSNNLNIPLGKKQKLTATGIYSDNSNR 259
QY 137 -----NLQNRGGIANYPRRTKVFNCVGDVCTGTLIITPAHL-SYVIE 179
Db 260 DISSSVIWNSSNSTIANIQNGILETADTGIVTSASTENIIGSVKLIIVTPAALVSISVS 319
QY 180 -ARGEAAFLRDRIRA 194
Db 320 PTNSTVAKGLQENFKA 335

RESULT 10

US-10-467-657-4396
; Sequence 4396, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4396
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4396

Query Match 7.5%; Score 75; DB 6; Length 481;
Best Local Similarity 22.9%; Pred. No. 8.8;
Matches 48; Conservative 24; Mismatches 82; Indels 56; Gaps 10;
QY 1 QLCRAIE-----NGLESGSANACPDAILIFARGSTE--PGNMGITVGPALA-- 43
Db 17 QISAVELASAVLAAIAEKNPALNGVITTDQDKTLAEARAADERIAQGNASALTGVVPVAK 76
QY 44 -----NGLESHIRNIWQVGGPYDAALATNPLPRG---TSQANIDEGKRLPALAN-- 91
Db 77 DIFCQTGWSACASAKMLDNFIFFYTATVQVQLLDGEMVTLGRTNNDE----FAMGSTNEN 132
QY 92 -----QKCP-NTPVWAGGYSGQAALIAAA-----VSELSGAVKEQVKGVALFGV--TQ 136
Db 133 SFYGAANKPNPHEVPGSGSGSAVVAARLAPALGSDTGCSTQINQAPASHCGITGKPTY 192
QY 137 NLQNRGGIANY-----PRRTKVFNCV 158
Db 193 GTVSRFCMWAVAYASSFDQAGPMAQTAEDCAI 222

RESULT 11

US-11-185-342-19
; Sequence 19, Application US/11185342
; Publication No. US20060021093A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Philip E.
; APPLICANT: Hinson, Todd K.
; APPLICANT: Carr, Brian
; APPLICANT: Duck, Nicholas B.
; TITLE OF INVENTION: GDC-1 GENES CONFERRING HERBICIDE
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 045600/275114
; CURRENT APPLICATION NUMBER: US/11/185,342
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: US/10/796,953
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: 60/453,237
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fungal isolate from soil sample
US-11-185-342-19

Query Match 7.5%; Score 75; DB 7; Length 575;
Best Local Similarity 26.1%; Pred. No. 11;
Matches 40; Conservative 18; Mismatches 65; Indels 30; Gaps 9;
QY 55 IQGVGGPYDAALATNPLPRGTSQANIDEGKRLPALANQKCPNTPVWAGGYSQ-----GAAL 110
Db 33 IHGLFGDYN-PLALDYLP-----SCGLRWGVSVEL--NAAVADGYARVKQWGLI 81
QY 111 IAAAVSELS-----GAVKEQVKGVALFGYTONLQNRGGIA---NYPRTKVFNCVGD 161
Db 82 TTFGVGELSAINGVAGAFSEHVPVHVIVGCCSTASQNRGMLLHHTLGLNGDFNIFAMMSAQ 141
QY 162 V-CTGTLLITPAHLSYTIAREGEAAR--FLDR 191

[illegible]

QY 181 RGEAARFLDRIRA 194
Db 404 SGEQTAVQDSVAA 417

RESULT 15
US-11-047-383-10
; Sequence 10, Application US/11047383
; Publication No. US20060003432A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: CLARKE, TERESA
; APPLICANT: KIMBER, MATHEW
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM ENTEROCOCCUS FAECALIS
; FILE REFERENCE: IPT-318.01
; CURRENT APPLICATION NUMBER: US/11/047,383
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: PCT/CA03/01135
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/400,435
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/453,405
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-047-383-10

Query Match 7.4%; Score 74; DB 7; Length 424;
Best Local Similarity 23.7%; Pred. No. 9.3;
Matches 46; Conservative 28; Mismatches 70; Indels 50; Gaps 13;
QY 30 EPGNMGITVGPALANGLESHIRNI--WI-----QG---VGGPYDAALATNFLPRGTSQA 78
Db 245 ESAGIAYTVNQRILVRGLDYNNRTVFENVNLSGSGQGTVCAGGRYD-GLVQLGGRATPAV 303
QY 79 NIDEG-KRLFAL---ANQKCPNPV-----AGGYSQGAALIAAAVSELGAVKEOVKG 128
Db 304 GFAMGLERLVLLVQAVNPEFKADPVVDIYLVASGADTQSAAM-----ALAEIRLDELPG 357
QY 129 VALFGYTQNLQNRGGIANYPRE-----RTKVFQCNVGDV-VCTGTLLIITPAHLSYITIA 180
Db 358 VKL-----MTNHGG-GNFKKQFARADKMGARVAVVLGESEVANGTAVVKDLR----- 403
QY 181 RGEAARFLDRIRA 194
Db 404 SGEQTAVQDSVAA 417

Search completed: February 4, 2006, 05:12:05
Job time : 16 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:57:14 ; Search time 600 Seconds
(without alignments)
446.832 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGATENGLESGSANACPD.....SYTIEARGEARFLRDIRA 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/1/paa/US066 COMB.pep.*
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- 4: /cgn2_6/ptodata/1/paa/US074 COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
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| 1 | 996 | 100.0 | 246 | 18 | US-08-817-997-2 | Sequence 2, Appli |
| 2 | 991 | 99.5 | 194 | 31 | US-10-152-300-1 | Sequence 1, Appli |
| 3 | 991 | 99.5 | 194 | 38 | US-10-846-123-1 | Sequence 1, Appli |
| 4 | 596 | 59.8 | 209 | 27 | US-09-791-537-26059 | Sequence 26059, A |
| 5 | 593.5 | 59.6 | 228 | 27 | US-09-791-537-32037 | Sequence 32037, A |
| 6 | 578 | 58.0 | 196 | 11 | US-08-171-805-59 | Sequence 59, Appl |
| 7 | 578 | 58.0 | 196 | 15 | US-08-551-983-64 | Sequence 64, Appl |
| 8 | 576 | 57.8 | 194 | 11 | US-08-171-805-57 | Sequence 57, Appl |
| 9 | 576 | 57.8 | 194 | 15 | US-08-551-983-62 | Sequence 62, Appl |
| 10 | 576 | 57.8 | 224 | 27 | US-09-791-537-55942 | Sequence 55942, A |
| 11 | 576 | 57.8 | 227 | 37 | US-10-703-032-168488 | Sequence 168488, A |
| 12 | 564 | 56.6 | 223 | 27 | US-09-791-537-55932 | Sequence 55932, A |
| 13 | 561 | 56.3 | 194 | 11 | US-08-171-805-58 | Sequence 58, Appl |
| 14 | 561 | 56.3 | 194 | 15 | US-08-551-983-63 | Sequence 63, Appl |
| 15 | 554 | 55.6 | 214 | 27 | US-09-791-537-17346 | Sequence 17346, A |
| 16 | 554 | 55.6 | 214 | 27 | US-09-791-537-17351 | Sequence 17351, A |
| 17 | 550.5 | 55.3 | 228 | 27 | US-09-791-537-55941 | Sequence 55941, A |
| 18 | 550 | 55.2 | 230 | 27 | US-09-791-537-102891 | Sequence 102891, A |
| 19 | 546 | 54.8 | 214 | 27 | US-09-791-537-132722 | Sequence 132722, A |
| 20 | 546 | 54.8 | 230 | 11 | US-08-100-586-43 | Sequence 43, Appl |
| 21 | 546 | 54.8 | 230 | 27 | US-09-791-537-114396 | Sequence 114396, A |
| 22 | 545.5 | 54.8 | 214 | 27 | US-09-791-537-127534 | Sequence 127534, A |
| 23 | 545 | 54.7 | 230 | 27 | US-09-791-537-55944 | Sequence 55944, A |
| 24 | 544 | 54.6 | 214 | 27 | US-09-791-537-17344 | Sequence 17344, A |
| 25 | 543.5 | 54.6 | 231 | 37 | US-10-703-032-105885 | Sequence 105885, A |
| 26 | 543 | 54.5 | 214 | 27 | US-09-791-537-17380 | Sequence 17380, A |
| 27 | 542.5 | 54.5 | 198 | 11 | US-08-171-805-56 | Sequence 56, Appl |
| 28 | 542.5 | 54.5 | 198 | 15 | US-08-551-983-61 | Sequence 61, Appl |
| 29 | 542.5 | 54.5 | 198 | 27 | US-09-791-537-21879 | Sequence 21879, A |
| 30 | 542.5 | 54.5 | 199 | 31 | US-10-152-300-2 | Sequence 2, Appli |
| 31 | 542.5 | 54.5 | 199 | 38 | US-10-846-123-2 | Sequence 2, Appli |
| 32 | 542.5 | 54.5 | 200 | 27 | US-09-791-537-6915 | Sequence 6915, Ap |
| 33 | 542.5 | 54.5 | 214 | 27 | US-09-791-537-74454 | Sequence 74454, A |
| 34 | 542.5 | 54.5 | 214 | 27 | US-09-791-537-127550 | Sequence 127550, A |
| 35 | 542.5 | 54.5 | 214 | 27 | US-09-791-537-127562 | Sequence 127562, A |
| 36 | 542 | 54.4 | 214 | 27 | US-09-791-537-17342 | Sequence 17342, A |
| 37 | 542 | 54.4 | 214 | 27 | US-09-791-537-17357 | Sequence 17357, A |
| 38 | 542 | 54.4 | 214 | 27 | US-09-791-537-128533 | Sequence 128533, A |
| 39 | 541.5 | 54.4 | 200 | 27 | US-09-791-537-27160 | Sequence 27160, A |
| 40 | 541.5 | 54.4 | 214 | 27 | US-09-791-537-127548 | Sequence 127548, A |
| 41 | 541.5 | 54.4 | 214 | 27 | US-09-791-537-127555 | Sequence 127555, A |
| 42 | 541.5 | 54.4 | 214 | 27 | US-09-791-537-127565 | Sequence 127565, A |
| 43 | 541 | 54.3 | 214 | 27 | US-09-791-537-17359 | Sequence 17359, A |
| 44 | 541 | 54.3 | 214 | 27 | US-09-791-537-17382 | Sequence 17382, A |
| 45 | 540 | 54.2 | 214 | 27 | US-09-791-537-17385 | Sequence 17385, A |

ALIGNMENTS

RESULT 1

US-08-817-997-2
; Sequence 2, Application US/08817997
; GENERAL INFORMATION:
; APPLICANT: Sandal, Thomas

```
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Kofod, Iene V.
; TITLE OF INVENTION: An Enzyme With Lipolytic
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk Of North America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,997
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4316.204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-817-997-2

Query Match      100.0%; Score 996; DB 18; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.7e-84;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINIWIQVGG 60
DB      36  OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINIWIQVGG 95
QY      61  PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSEL 120
DB      96  PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSEL 155
QY      121 AVKEQVKGVALLFGYTQNLQNRGGIANYPRETRKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180
DB      156 AVKEQVKGVALLFGYTQNLQNRGGIANYPRETRKVFNCVGDVAVCTGTLITPAHLSYTTIEA 215
QY      181 RGEAARFLDRIRA 194
DB      216 RGEAARFLDRIRA 229

RESULT 2
US-10-152-300-1
; Sequence 1, Application US/10152300
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Sticksies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Humicola insolens
US-10-152-300-1

Query Match      99.5%; Score 991; DB 38; Length 194;
Best Local Similarity 99.5%; Pred. No. 3.4e-84;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINIWIQVGG 60
DB      1  OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINIWIQVGG 60
QY      61  PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSEL 120
DB      61  PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSEL 120
QY      121 AVKEQVKGVALLFGYTQNLQNRGGIANYPRETRKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180
DB      121 AVKEQVKGVALLFGYTQNLQNRGGIANYPRETRKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180
QY      181 RGEAARFLDRIRA 194
DB      181 RGEAARFLDRIRA 194

RESULT 3
US-10-846-123-1
; Sequence 1, Application US/10846123
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Sticksies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/846,123
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Humicola insolens
US-10-846-123-1

Query Match      99.5%; Score 991; DB 38; Length 194;
Best Local Similarity 99.5%; Pred. No. 3.4e-84;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINIWIQVGG 60
DB      1  OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINIWIQVGG 60
QY      61  PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSEL 120
DB      61  PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSEL 120
QY      121 AVKEQVKGVALLFGYTQNLQNRGGIANYPRETRKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180
DB      121 AVKEQVKGVALLFGYTQNLQNRGGIANYPRETRKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180
QY      181 RGEAARFLDRIRA 194
DB      181 RGEAARFLDRIRA 194
```

RESULT 4
US-09-791-537-26059
; Sequence 26059, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26059
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Alternaria brassicicola
US-09-791-537-26059

Query Match 59.8%; Score 596; DB 27; Length 209;
Best Local Similarity 60.3%; Pred. No. 5.1e-47;
Matches 117; Conservative 22; Mismatches 53; Indels 2; Gaps 1;

QY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLES--HIRNIWQGV 58
DB 13 QASTTRNELETGSSDACPRITIFIFARGSTPGNMGITVGPALANGLES--HIRNIWQGV 72
QY 59 GGPYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSEL 118
DB 73 GGPYTAGLVENALPAGTSQAAREARQLFNLAASKCPNTPTITAGGYSQGAALIAAAVSEL 132
QY 119 SGAVKEOVKGVALFGYTONLQNRGGIANYPRTKVFNCNVGDVAVCTGTLITPAHLSTYIE 178
DB 133 SAAVQDIKGVVLFGYTKLQNRGRIPDPFTKTEVCYNASDAVCFGLFLPAHLSTYIE 192
QY 179 EARGEAAFLDRIR 192
DB 193 EAAVQAPTEFLRAQI 206

RESULT 5
US-09-791-537-32037
; Sequence 32037, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32037
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pyricularia grisea
US-09-791-537-32037

Query Match 59.6%; Score 593.5; DB 27; Length 228;
Best Local Similarity 59.5%; Pred. No. 9.9e-47;
Matches 116; Conservative 27; Mismatches 51; Indels 1; Gaps 1;

QY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLES--HIRNIWQGV 59
DB 33 QLNVRNDLISGNAACPSVILLIFARASGEVGNMGLSAGTNVARSRLERFRNDIWWQGV 92
QY 60 GPYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSEL 119
DB 93 DPYDAALSPNPLPAGTTQGAIDEAKRMFTLANTKCPNAAVAVAGGYSQGTAVMNAVSEMP 152

QY 120 GAVKEOVKGVALFGYTONLQNRGGIANYPRTKVFNCNVGDVAVCTGTLITPAHLSTYIE 179
DB 153 AAVQDIKGVVLFGYTKLQNRGRIPDPFTKTEVCYNASDAVCFGLFLPAHLSTYIE 212
QY 180 ARGEAAARFLDRIR 194
DB 213 SSIAAPNWLIRQIRA 227

RESULT 6

US-08-171-805-59
; Sequence 59, Application US/08171805
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert
; APPLICANT: VAN DER HUIJZEN, Hendrikus Theodorus W.M.
; APPLICANT: MUSTERS, Wouter
; APPLICANT: PETERS, Hans
; APPLICANT: VERRIPS, Cornelis Theodorus
; APPLICANT: DE Vlieg, Jakob
; TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
; STREET: 45 RIVER ROAD
; CITY: EDGEWATER
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171.805
FILING DATE: 22-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Koatz, Ronald A.
REGISTRATION NUMBER: 31,774
REFERENCE/DOCKET NUMBER: 93-0065-A-UNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 943-7100
TELEFAX: (201) 943-3661
TELEX: 640 333 LEVER EDGE
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-171-805-59

Query Match 58.0%; Score 578; DB 11; Length 196;
Best Local Similarity 57.9%; Pred. No. 2.3e-45;
Matches 113; Conservative 28; Mismatches 52; Indels 2; Gaps 1;

QY 2 LGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLES--HIRNIWQGV 59
DB 1 LNSVRNDLISGNAACPSVILLIFARASGEVGNMGLSAGTNVARSRLERFRNDIWWQGV 60
QY 60 GPYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSEL 119
DB 61 DPYDAALSPNPLPAGTTQGAIDEAKRMFTLANTKCPNAAVAVAGGYSQGTAVMNAVSEMP 120
QY 120 GAVKEOVKGVALFGYTONLQNRGGIANYPRTKVFNCNVGDVAVCTGTLITPAHLSTYIE 179
DB 121 AAVQDIKGVVLFGYTKLQNRGRIPDPFTKTEVCYNASDAVCFGLFLPAHLSTYIE 180
QY 180 ARGEAAARFLDRIR 194

Db 181 SSIAAPNWLIRQIRA 195

RESULT 7

US-08-551-983-64
; Sequence 64, Application US/08551983
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert
; APPLICANT: VAN DER HIJDEN, Hendrikus Theodorus W.M.
; APPLICANT: MUSTERS, Wouter
; APPLICANT: PETERS, Hans
; APPLICANT: VERRIPS, Cornelis Theodorus
; TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
; STREET: 45 RIVER ROAD
; CITY: EDGEWATER
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07020

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551,983
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,803
; FILING DATE: 17-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Koatz, Ronald A.
; REGISTRATION NUMBER: 31,774
; REFERENCE/DOCKET NUMBER: 93-0064-A-UNI

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 943-7100
; TELEFAX: (201) 943-3661
; TELEX: 640 333 LEVER EDGE
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 196 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-551-983-64

Query Match 58.0%; Score 578; DB 15; Length 196;
Best Local Similarity 57.9%; Pred. No. 2.3e-45;
Matches 113; Conservative 28; Mismatches 52; Indels 2; Gaps 1;

QY 2 LGAIENLSEGSANACPDAILIFARGSTEPGNMGITVGPALANGLSHI--RNINIQGVG 59
Db 1 LNSVRNDLSGNAACPSVILIFARASGEVGNMGLSAGTNVASRLERFGRNDIIVQGVG 60
QY 60 GPYDAALATNLFPRGTGTSQANIDEGKRLFALANOKCPNTFPVAGYSQGAALIAAAVSELS 119
Db 61 DPYDAALSNFLPAGTITQGAIDAKGMFTLTANTKCPNAAVVAGYSQGTAVMFAVSEMP 120
QY 120 GAVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCNVDGAVCTGTLLITPAHLSYTIIE 179
Db 121 AAQDDQIKGVWLFQYTKNLQNRGRI PDPFTEKTEVYCNASDAVCFGLFLPFAHFLYTTIE 180
QY 180 ARGEAAARFLDRIRA 194
Db 181 SSIAAPNWLIRQIRA 195

RESULT 8

US-08-171-805-57
; Sequence 57, Application US/08171805
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert
; APPLICANT: VAN DER HIJDEN, Hendrikus Theodorus W.M.
; APPLICANT: MUSTERS, Wouter
; APPLICANT: PETERS, Hans
; APPLICANT: VERRIPS, Cornelis Theodorus
; APPLICANT: DE Vlieg, Jakob
; TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
; STREET: 45 RIVER ROAD
; CITY: EDGEWATER
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07020

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,805
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Koatz, Ronald A.
; REGISTRATION NUMBER: 31,774
; REFERENCE/DOCKET NUMBER: 93-0065-A-UNI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 943-7100
; TELEFAX: (201) 943-3661
; TELEX: 640 333 LEVER EDGE
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-171-805-57

Query Match 57.8%; Score 576; DB 11; Length 194;
Best Local Similarity 58.5%; Pred. No. 3.5e-45;
Matches 110; Conservative 28; Mismatches 48; Indels 2; Gaps 1;

QY 7 NGLSEGSANACPDAILIFARGSTEPGNMGITVGPALANGLS--HIRNIWQGVGYPDA 64
Db 6 NELETSSSACPKVIYIFARASTEPGNMGISAGFIVADALERIYCANNVWQGVGYPILA 65
QY 65 ALATNLFPRGTGTSQANIDEGKRLFALANOKCPNTFPVAGYSQGAALIAAAVSELSGAVKE 124
Db 66 DLASNFLPDGTSSAAINEARLFLANTKCPNAAIVSGYSGQGTAVMAGSISGLSTTIKN 125
QY 125 QVKGVALFGYTONLQNRGGIANYPRRTKVFNCNVDGAVCTGTLLITPAHLSYTIIEARGEA 184
Db 126 QIKGVWLFQYTKNLQNLGRIPNFTSKTEVYCIADAVCYGTLFILPAHFLYQTDAAVAA 185
QY 185 ARFLDRIRI 192
Db 186 PRELQARI 193

RESULT 9

US-08-551-983-62
; Sequence 62, Application US/08551983
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert

APPLICANT: VAN DER HILDEN, Hendrikus Theodorus W.M.
APPLICANT: MUSTERS, Wouter
APPLICANT: PETERS, Hans
APPLICANT: VERRIPS, Cornelis Theodorus
APPLICANT: DE VLEG, Jakob
TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
STREET: 45 RIVER ROAD
CITY: EDGEWATER
STATE: N.J.
COUNTRY: USA
ZIP: 07020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,983
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,803
FILING DATE: 17-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Koatz, Ronald A.

REGISTRATION NUMBER: 31,774
REFERENCE/DOCKET NUMBER: 93-0064-A-UNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 943-7100
TELEFAX: (201) 943-3661

TELEX: 640 333 LEVER EDGE
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-551-983-62

Query Match 57.8%; Score 576; DB 15; Length 194;
Best Local Similarity 58.5%; Pred. No. 3.5e-45;
Matches 110; Conservative 28; Mismatches 48; Indels 2; Gaps 1;

Qy 7 NLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLES--HIRNIWIOGVGGPYDA 64
Db 6 NELETSSSACPKVIYIFARASTPEGNMGISAGPIVADALERIYGANNVWVGVPYLA 65
Qy 65 ALATNPLRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSELGAVKE 124
Db 66 DLASNFLPDGTSSAINEARLFTLANTKCPNAAIVSGGYSQGTAVMAGSISGLSTTKN 125
Qy 125 QVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGLTIITPAHLSYTIARGEA 184
Db 126 QIKGVWLFYTKNLQNLGRIPNFTSKTEVYCDIADAVCYGTLFILPAHFLYQTDAAVAA 185

Qy 185 ARFLRDRI 192
Db 186 PRFLQARI 193

RESULT 10
US-09-791-537-55942
GENERAL INFORMATION:
APPLICATION US/09791537

APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB

TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patent in version 3.0
SEQ ID NO 55942
LENGTH: 224
TYPE: PRT
ORGANISM: Colletotrichum gloeosporioides
US-09-791-537-55942

Query Match 57.8%; Score 576; DB 27; Length 224;
Best Local Similarity 58.5%; Pred. No. 4.3e-45;
Matches 110; Conservative 28; Mismatches 48; Indels 2; Gaps 1;

Qy 7 NLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLES--HIRNIWIOGVGGPYDA 64
Db 36 NELETSSSACPKVIYIFARASTPEGNMGISAGPIVADALERIYGANNVWVGVPYLA 95
Qy 65 ALATNPLRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSELGAVKE 124
Db 96 DLASNFLPDGTSSAINEARLFTLANTKCPNAAIVSGGYSQGTAVMAGSISGLSTTKN 155
Qy 125 QVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGLTIITPAHLSYTIARGEA 184
Db 156 QIKGVWLFYTKNLQNLGRIPNFTSKTEVYCDIADAVCYGTLFILPAHFLYQTDAAVAA 215
Qy 185 ARFLRDRI 192
Db 216 PRFLQARI 223

RESULT 11

US-10-703-032-168488

Sequence 168488, Application US/10703032
GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Andersen, Scott E.
APPLICANT: Byrum, Joseph R.
APPLICANT: Conner, Timothy W.
APPLICANT: Cao, Yongwei
APPLICANT: Masucci, James D.
APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(53374)B
CURRENT APPLICATION NUMBER: US/10/703.032
CURRENT FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: 10/020,338
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 211164
SEQ ID NO 168488
LENGTH: 227
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:

OTHER INFORMATION: Clone ID: PAT_TA_62906.pap
US-10-703-032-168488

Query Match 57.8%; Score 576; DB 37; Length 227;
Best Local Similarity 58.9%; Pred. No. 4.4e-45;
Matches 116; Conservative 27; Mismatches 50; Indels 4; Gaps 3;

Qy 1 QLGA1-ENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHI--RNIWIOG 57
Db 30 QAGSITRNDLSSGASSACPPVIFYARGSTELNGL-TLGPVSALESYYGRDKVIOG 88
Qy 58 VGGPYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSE 117
Db 89 VGGAYDATIGDNLPRGTSAAIREMIALFNLANSKCPSAKVAGGYSQGAALAAASIED 148
Qy 118 LSGAVKEQVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGLTIITPAHLSY 177

Db 149 LSTSVRDKVGTVLFGYTKNLQNLGRIPNYPRRTKVFNCIGDLVCTGSLVAAAPHLAYQ 208
Qy 178 IEARGEAAARFLDRIRA 194
Db 209 SDASGPAPFLQIRVAA 225

RESULT 12
US-09-791-537-55932
; Sequence 55932, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55932
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Ascochyta rabiei
US-09-791-537-55932

Query Match 56.6%; Score 564; DB 27; Length 223;
Best Local Similarity 58.6%; Pred. No. 5.7e-44;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

Qy 5 IEENGESGANACPDAILIFARGSTEPGNMGITVGPALANGLESH-IRNIWIQVGGPYD 63
Db 34 IRSELEQSSSSCPKAILIFARGSTIEGNMGVSNAGPAVASALEAYGADQIWWQVGGPYT 93
Qy 64 AALATNPLRGTSQANIDEGKRLFALANOKPNTPVVGYSQGAALIAAAVSELGAVK 123
Db 94 ADLPSNPLPGGTSQAINAEAVRLFNEANTKCPSTPIVAGYSQGTAVMAGAIPKLD-AVR 152
Qy 124 EQKGVALLFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLIITPAHLSYTIPEARSE 183
Db 153 ARVGVTVLFGYTONQNNKGIKDYPQEDLQVYCEVGDVCDGTLLITVSHFLYLEEAAAP 212
Qy 184 AARFLDRIRA 194
Db 213 APEFLKSKIGA 223

RESULT 13
US-08-171-805-58
; Sequence 58, Application US/08171805
; GENERAL INFORMATION:
; APPLICANT: EGOMOND, Maarten Robert
; APPLICANT: VAN DER HIJDEN, Hendrikus Theodorus W.M.
; APPLICANT: MUSTERS, Wouter
; APPLICANT: PETERS, Hans
; APPLICANT: VERRIPS, Cornelis Theodorus
; APPLICANT: DE Vlieg, Jakob
; TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
; STREET: 45 RIVER ROAD
; CITY: EDGEWATER
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

FILING DATE: 17-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Koatz, Ronald A.
REGISTRATION NUMBER: 31, 774
REFERENCE/DOCKET NUMBER: 93-0064-A-UNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 943-7100
TELEFAX: (201) 943-3661
TELEX: 640 333 LEVER EDGE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-551-983-63

Query Match
Best Local Similarity 56.3%; Score 561; DB 15; Length 194;
Matches 108; Conservative 27; Mismatches 51; Indels 2; Gaps 1;

QY 7 NGLSSANACPDAILIFARGSTPGNMGITVGPALANGLESH--IRNIWQVGGPYDA 64
DB 6 NELESGSSNCPKVIYIFARASTPGNMGISAGPIVADALESRYGASQVWVQVGGPYSA 65
QY 65 ALATNPLPGTQANIDEGRKLFALANQKCPNTPVWAGGYSQGAALIAAAVSELSGAVKE 124
DB 66 DLANFIPEGTSRVAINAKRLFTLANTKCPNSAVVAGGYSQGTAVWASSISELSSTION 125
QY 125 QVKGVALFGYTONLQNRGGIANYPRETRKVFNCNVGDAVCTGTLIITPAHLSYTTIARGEA 184
DB 126 QIKGVLSAITKQLNGLRIPNFTSKTEVYCALADAVCYGTLFILPAHFLYQADAATSA 185
QY 185 ARFLDRRI 192
DB 186 PRELAARI 193

RESULT 15
US-09-791-537-17346
Sequence 17346, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17346
LENGTH: 214
TYPE: PRT
ORGANISM: pdb 1CUWA
US-09-791-537-17346

Query Match
Best Local Similarity 55.6%; Score 554; DB 27; Length 214;
Matches 110; Conservative 31; Mismatches 52; Indels 4; Gaps 3;

QY 1 QLG-AIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESHI--RNIWIQ 57
DB 14 QLGRTTRDDLINGSASCADVIFYARGSTETGNLG-TLGPSTASNLESFQKDGWVIQ 72
QY 58 VCGPYDAALATNPLPGTQANIDEGRKLFALANQKCPNTPVWAGGYSQGAALIAAVSE 117
DB 73 VGGAYRATLADNPLPRGTSAAIREMLGLFQANTKCPDATLIAGGYSQGAALAAASIED 132
QY 118 LSGAVKEQVKGVALFGYTONLQNRGGIANYPRETRKVFNCNVGDAVCTGTLIITPAHLSYT 177

Db 133 LDSAIRDKIAGTVLFGYTKNLQNRGRIPNYPADRTKVFCTGDLVCTGSLIILAPHFAYG 192
QY 178 IEARGEAAARFLDRIRA 194
DB 193 PDARGPAPEFLIEKVRA 209

Search completed: February 4, 2006, 05:07:58
Job time : 601 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2006, 04:58:04 ; Search time 35 Seconds
(without alignments)
385.289 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGATENGLESANACPDPA.....SYTIARGEARPLRDRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 259879 seqs, 69510979 residues

Total number of hits satisfying chosen parameters: 259879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*

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7: /cgn2_6/prodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 242.5 | 24.3 | 686 | 1 | PCT-US06-00964-8187 |
| 2 | 242.5 | 24.3 | 686 | 7 | US-11-330-403-8187 |
| 3 | 234.5 | 23.5 | 1003 | 1 | PCT-US06-00964-10079 |
| 4 | 234.5 | 23.5 | 1003 | 7 | US-11-330-403-10079 |
| 5 | 88 | 8.8 | 1356 | 8 | US-60-752-355-22033 |
| 6 | 87 | 8.7 | 1356 | 8 | US-60-752-355-5682 |
| 7 | 87 | 8.7 | 1356 | 8 | US-60-752-355-5686 |
| 8 | 87 | 8.7 | 1356 | 8 | US-60-752-355-5687 |
| 9 | 86.5 | 8.7 | 649 | 7 | US-11-311-940-9837 |
| 10 | 86 | 8.6 | 1331 | 7 | US-11-311-940-5856 |
| 11 | 85 | 8.5 | 7510 | 8 | US-60-752-355-12835 |
| 12 | 84.5 | 8.5 | 628 | 1 | PCT-US06-00964-1798 |
| 13 | 84.5 | 8.5 | 628 | 7 | US-11-330-403-1798 |
| 14 | 84.5 | 8.5 | 772 | 8 | US-60-752-355-22380 |
| 15 | 84.5 | 8.5 | 1376 | 8 | US-60-752-355-5711 |
| 16 | 84.5 | 8.5 | 2082 | 1 | PCT-US06-00964-9531 |
| 17 | 84.5 | 8.5 | 2082 | 7 | US-11-330-403-9531 |
| 18 | 82 | 8.2 | 1424 | 7 | US-11-311-940-8349 |
| 19 | 80 | 8.0 | 440 | 7 | US-11-311-940-7587 |
| 20 | 80 | 8.0 | 515 | 1 | PCT-US06-00964-18288 |
| 21 | 80 | 8.0 | 515 | 7 | US-11-330-403-18288 |
| 22 | 80 | 8.0 | 653 | 6 | US-10-953-349-33827 |
| 23 | 80 | 8.0 | 784 | 6 | US-10-953-349-33826 |
| 24 | 80 | 8.0 | 841 | 6 | US-10-953-349-33825 |
| 25 | 79.5 | 8.0 | 545 | 8 | US-60-752-355-48339 |

Sequence 20, Appl
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Sequence 21315, A
Sequence 5952, Ap
Sequence 4963, Ap
Sequence 5687, Ap
Sequence 1993, Ap
Sequence 1992, Ap
Sequence 1991, Ap
Sequence 1325, Ap
Sequence 1325, Ap
Sequence 14, Appl
Sequence 6292, Ap
Sequence 14726, A
Sequence 6292, Ap
Sequence 14726, A
Sequence 4514, Ap
Sequence 46534, A
Sequence 9830, Ap

26 79 296 7 US-11-246-957-20
27 79 298 8 US-60-752-355-47282
28 79 311 8 US-60-752-355-21315
29 79 441 7 US-11-311-940-5952
30 79 442 7 US-11-311-940-4963
31 79 462 7 US-11-311-940-5687
32 78.5 303 6 US-10-953-349-1993
33 78.5 377 6 US-10-953-349-1992
34 78.5 382 6 US-10-953-349-1991
35 78.5 411 8 US-60-752-355-36639
36 78.5 1536 1 PCT-US06-00964-1325
37 78.5 7 1536 7 US-11-330-403-1325
38 78 297 7 US-11-246-957-14
39 78 424 1 PCT-US06-00964-6292
40 78 424 1 PCT-US06-00964-14726
41 78 424 7 US-11-330-403-6292
42 78 424 7 US-11-330-403-14726
43 78 470 8 US-60-752-355-4514
44 77.5 385 8 US-60-752-355-46534
45 77.5 497 1 PCT-US06-00964-9830

ALIGNMENTS

RESULT 1

PCT-US06-00964-8187

; Sequence 8187, Application PC/TUS0600964

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53629)B

; CURRENT APPLICATION NUMBER: PCT/US06/00964

; CURRENT FILING DATE: 2006-01-23

; NUMBER OF SEQ ID NOS: 19250

; SEQ ID NO 8187

; LENGTH: 686

; TYPE: PRT

; ORGANISM: ASPERGILLUS NIDULANS FGSC A4

PCT-US06-00964-8187

Query Match 24.3%; Score 242.5; DB 1; Length 686;

Best Local Similarity 37.4%; Pred. No. 1.2e-13;

Matches 76; Conservative 25; Mismatches 67; Indels 35; Gaps 10;

Qy 2 LGATENG...ESGSA-----NACPDAILIFARGSTEGNMGITVGPALANGLESHI 50
Db 497 LGKLPRALGKRSRSGSSTNDVTNSGCKELTFIFARGTTEIGNMTVTVPKVGKALKSLT 556
Qy 51 RN-IWIOGVGYPYDAALATNPLPRGTSQANIDEGKRLPAL---ANQKCPNTPVAVGGYSQ 106
Db 557 GNKAAIOGVDPADAA-----GNAALGGSGGPKMASLVETALKQCPDTKIVLGGYSQ 608
Qy 107 GAALIAAANSELGAVKEQKGVNLTQNLQNRGGIANYPRETKYFCNVGDVAVC-TG 165
Db 609 GAVVHNAASKLSGG---QVVGAVTFGDPFKSQPDNI-----DQFKTFCASGDPVCLNG 660
Qy 166 TLITPAHLSVYTEARGEARFL 188
Db 661 ANVM--AHLGYGNDAAQ-TAAQFL 680

RESULT 2

US-11-330-403-8187

; Sequence 8187, Application US/11330403

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53629)B

; CURRENT APPLICATION NUMBER: US/11/330,403

; CURRENT FILING DATE: 2006-01-12

; NUMBER OF SEQ ID NOS: 19250

; SEQ ID NO 8187

Db 329 NTWDTLSAFADVTRVAREVGTGRGCGQANVPNVAGTWKDLTDNVSMANNTNQVRN 388
Qy 53 IWIQGVGPGYDAALATNPLRGTSQANIDEGKRLFALANOKCPNTPV-VAGGYSQGAALI 111
Db 389 I-----ALVTTAVARGDLKKLDVARGILELKTINTWVDLSAFADVTRV 437
Qy 112 AAUV-----SELGAVKEQVGVGVALFGYTNL-QNRGGIANYPRTKVFNCVGDVCTGTL 167
Db 438 AREVTEGRGG--QAEVEGVS--GTWKRLTENNELAGNLTRQVRAIEVTSVAEGDL 493
Qy 168 IITPAHLSYTIAREGEAARFLDRRA 194
Db 494 T-----RSVTVEASGEVAE-LGDNINA 514

RESULT 11

US-60-752-355-12835
; Sequence 12835, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)B
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12835
; LENGTH: 7510
; TYPE: PRT
; ORGANISM: Streptomyces aizunensis
US-60-752-355-12835

Query Match 8.5%; Score 85; DB 8; Length 7510;

Best Local Similarity 24.2%; Pred. No. 3.6e+02; Mismatches 85; Indels 54; Gaps 11; Matches 54; Conservative 30;

Qy 1 OLGAIENTGLE-----SGSANACPDAILIFARGSTEGPNCMGITVGPALANGL-----ESHI 50
Db 1964 RLPVPEGLEGLGTGTAGSVASGRISYTFGLEGP---AVTDTACSSSLVALHLAAQAL 2020
Qy 51 RNIWITQGVGPGYDAALATNPLRGTSQANIDEGKRLFALANOKCPNTPVAG--GYSQGA 108
Db 2021 RN-----GECDMALAGGVTVMTPTDFTDFSRQKGLSGNGRCKSFSDADGTGWAGA 2073
Qy 109 ALIAAAVSELSCA-----VKEQVGVGVALFGYTNLQNRGGIAN-----YPRRTK 153
Db 2074 GMI--LVERLSDRNRHGHQVLAVVRGTAV-----NODGASNGITAPNPSQQRVIRQ 2123
Qy 154 VPCNVGDVCTGTLITPAH-----LSYTIAREGEAARFLDR 191
Db 2124 ALANAG--LTTAEVDVVEAHGTGTLGDPIEAQALLATYQDR 2164

RESULT 12

PCT-US06-00964-1798
; Sequence 1798, Application PC/TUS0600964
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: PCT/US06/00964
; CURRENT FILING DATE: 2006-01-23
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 1798
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
PCT-US06-00964-1798

Query Match 8.5%; Score 84.5; DB 1; Length 628;

Best Local Similarity 18.8%; Pred. No. 14; Mismatches 66; Indels 53; Gaps 7; Matches 37; Conservative 41;

Qy 13 SANACPDAILIFARGSTEGPNCMGITVGPALANGLSHIRNIWITQGVGPGYDAALATNPLP 72
Db 427 SSDVILDPLLSLRKGLAVPGDVKVSVDNIIIKVVAALRNV-----P 468
Qy 73 RGTQSANIDEGKRL-----FALANOKCPNTPVAGGYSQGAALIAAAVSELSGAVKE 124
Db 469 ENAYVNVVEKGEVVLVNDSDICIAVATEKGLMTPIIKNADOKTISAISSSEVKELAAKARA 528
Qy 125 -QVKGVALFGYTNLQNRGGIANYPRTKVFNCVGD-----AVCTGTLLIITP----- 171
Db 529 GKLPHEFGQGTFSINLQ---MFPVDK---FCAIINPPQACILAVGRGNKVVEPVGTD 582
Qy 172 -----AHLSTYIEA 180
Db 583 GIEKPSIATKLSLTLA 599

RESULT 13

US-11-330-403-1798
; Sequence 1798, Application US/11330403
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 1798
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-1798

Query Match 8.5%; Score 84.5; DB 7; Length 628;

Best Local Similarity 18.8%; Pred. No. 14; Mismatches 66; Indels 53; Gaps 7; Matches 37; Conservative 41;

Qy 13 SANACPDAILIFARGSTEGPNCMGITVGPALANGLSHIRNIWITQGVGPGYDAALATNPLP 72
Db 427 SSDVILDPLLSLRKGLAVPGDVKVSVDNIIIKVVAALRNV-----P 468
Qy 73 RGTQSANIDEGKRL-----FALANOKCPNTPVAGGYSQGAALIAAAVSELSGAVKE 124
Db 469 ENAYVNVVEKGEVVLVNDSDICIAVATEKGLMTPIIKNADOKTISAISSSEVKELAAKARA 528
Qy 125 -QVKGVALFGYTNLQNRGGIANYPRTKVFNCVGD-----AVCTGTLLIITP----- 171
Db 529 GKLPHEFGQGTFSINLQ---MFPVDK---FCAIINPPQACILAVGRGNKVVEPVGTD 582
Qy 172 -----AHLSTYIEA 180
Db 583 GIEKPSIATKLSLTLA 599

RESULT 14

US-60-752-355-22380
; Sequence 22380, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)B
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22380
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Magnetospirillum gryphiswaldense
US-60-752-355-22380

Query Match 8.5%; Score 84.5; DB 8; Length 772;

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Best Local Similarity 25.8%; Pred. No. 18;
Matches 39; Conservative 17; Mismatches 56; Indels 39; Gaps 8;

QY 12 GSANACPDAILIFARG-----STEPGNMGITV-GPALANGLESHIRNIWIQGVGGPYD 63
Db 496 GSVGAAP-----IAAPGAGGAYRFPQPGSLAINIQGPRGQGA-----VAGSGGSRA 543
QY 64 AALATNPLP---RGTQANIDEGKRLPALANQKCPNTPVAVGGYSQGAAL-----110
Db 544 SLIGAALTTLTQRLGLQANLPAGRGVP--VNGVTNTPPAASAGLRPGDVILKVDGRFVHQ 601
QY 111 ---IAAAVSELGAVKEQVKVALFGVTONL 138
Db 602 PEEVAIAEMPNRGRSVRI-GVLRAGDVSNM 631

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```

RESULT 15
US-60-752-355-5711
; Sequence 5711, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)B
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5711
; LENGTH: 1376
; TYPE: PRT
; ORGANISM: Podospora anserina
US-60-752-355-5711

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Query Match 8.5%; Score 84.5; DB 8; Length 1376;
Best Local Similarity 24.0%; Pred. No. 40;
Matches 47; Conservative 27; Mismatches 77; Indels 45; Gaps 10;

QY 11 GSANACPDAILIF--ARGs---TEPGNMG-----ITVGP-----LANGLESHIRNIW---- 54
Db 974 SGSADS---TIKIWEAATGCTQTLEGGHGPVNSVAFSPDSKWSGSDHDTIKIWEAAT 1030
QY 55 -----IQGVGGPYDAALATNPLP--RGTQANIDEGKRLPALANQKCPNTPVAVGGYSQ 106
Db 1031 GSCTQTLEGGHGPVN---SVTFSPDSKWSGSDHDTIKIWEAATGCTQTLEGGHGWY 1087
QY 107 GAALIAAAVSELGAVKEQVK--GVALFGVTONLQNRGG-----IANYPRER 151
Db 1088 SVAFSPDSKWSVSGSADSTIKIWEAATGCTQTLEGGHGSVNSVAFSPDSKWSGSDTR 1147
QY 152 TKVFCNVGDVACTGTL 167
Db 1148 TIKIWEAATGCTQTIL 1163

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Search completed: February 4, 2006, 05:08:40
Job time : 36 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, (using frame plus_p2n_model)

Run on: February 4, 2006, 21:44:24 ; Search time 4847 Seconds
(without alignments)
2275.145 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGATENGLESANACPD.....SYTIERGEARFLDRIRA 194

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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10: gb.sts.*
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12: gb.un.*
13: gb.vi.*
14: gb.hg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 991 | 99.5 | 994 | 6 | AR050618 Sequence |
| 2 | 552 | 55.4 | 1545 | 15 | ABU03393 |
| 3 | 546 | 54.8 | 718 | 6 | A36991 Sequence 42 |

| | | | | | |
|----|-------|------|--------|----|----------|
| 4 | 546 | 54.8 | 718 | 6 | A39199 |
| 5 | 546 | 54.8 | 718 | 6 | A39258 |
| 6 | 546 | 54.8 | 1121 | 6 | A00975 |
| 7 | 545 | 54.7 | 883 | 15 | FSOCUT |
| 8 | 544.5 | 54.7 | 1749 | 15 | COGCUA |
| 9 | 539.5 | 54.2 | 5768 | 15 | AF444194 |
| 10 | 531.5 | 53.4 | 3938 | 15 | FSU63335 |
| 11 | 531 | 53.3 | 2557 | 15 | COGCUA |
| 12 | 519.5 | 52.2 | 1735 | 15 | AF417004 |
| 13 | 519.5 | 52.2 | 2769 | 15 | FSOCUT |
| 14 | 518.5 | 52.0 | 1662 | 15 | ARCUT |
| 15 | 517.5 | 52.0 | 1697 | 15 | AF417005 |
| 16 | 517 | 51.9 | 2049 | 15 | MGCTT1 |
| 17 | 506 | 50.8 | 789 | 6 | CO788695 |
| 18 | 500.5 | 50.3 | 914 | 6 | ARI95188 |
| 19 | 499.5 | 50.2 | 999 | 6 | ARI95190 |
| 20 | 482 | 48.4 | 869 | 6 | ARI95189 |
| 21 | 430 | 43.2 | 2371 | 6 | CO788694 |
| 22 | 388.5 | 39.0 | 1350 | 15 | ASNC |
| 23 | 262 | 26.3 | 280 | 6 | A36990 |
| 24 | 262 | 26.3 | 280 | 6 | A39198 |
| 25 | 262 | 26.3 | 280 | 6 | A39257 |
| 26 | 260 | 26.1 | 768 | 6 | AX767352 |
| 27 | 260 | 26.1 | 798 | 6 | BD184000 |
| 28 | 260 | 26.1 | 798 | 6 | AR300500 |
| 29 | 260 | 26.1 | 798 | 6 | AR594235 |
| 30 | 260 | 26.1 | 798 | 6 | AR613466 |
| 31 | 260 | 26.1 | 798 | 6 | AR647284 |
| 32 | 260 | 26.1 | 798 | 6 | AX453426 |
| 33 | 260 | 26.1 | 798 | 6 | BD004787 |
| 34 | 229.5 | 23.0 | 1177 | 15 | AF305598 |
| 35 | 212 | 21.3 | 246 | 6 | A36975 |
| 36 | 212 | 21.3 | 246 | 6 | A39183 |
| 37 | 212 | 21.3 | 246 | 6 | A39242 |
| 38 | 210 | 21.1 | 2848 | 15 | BCUTAGN |
| 39 | 195 | 19.6 | 819 | 15 | AY954247 |
| 40 | 193 | 19.4 | 289308 | 1 | AE017242 |
| 41 | 192 | 19.3 | 1025 | 15 | AB039325 |
| 42 | 189.5 | 19.0 | 651 | 6 | AR456004 |
| 43 | 189.5 | 19.0 | 654 | 6 | BD273847 |
| 44 | 189.5 | 19.0 | 654 | 6 | AX005139 |
| 45 | 189.5 | 19.0 | 720 | 6 | BD273848 |

ALIGNMENTS

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| RESULT 1 | AR050618 | Sequence 1 from patent US 5827719. | 994 bp | DNA | linear | PAT 29-SEP-1999 |
| AR050618 | LOCUS | | | | | |
| DEFINITION | Sequence 1 from patent US 5827719. | | | | | |
| ACCESSION | AR050618 | | | | | |
| VERSION | AR050618.1 | GI:5973343 | | | | |
| KEYWORDS | Unknown. | | | | | |
| SOURCE | Unknown. | | | | | |
| ORGANISM | Unknown. | | | | | |
| REFERENCE | 1 (bases 1 to 994) | | | | | |
| AUTHORS | Sandal, T., Kauppinen, S. and Kofod, L. Venke. | | | | | |
| TITLE | Enzyme with lipolytic activity | | | | | |
| JOURNAL | Patent: US 5827719-A 1 27-OCT-1998; | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| source | 1. .994 | | | | | |
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| | /mol_type="unassigned DNA" | | | | | |
| ORIGIN | | | | | | |
| Alignment Scores: | | | | | | |
| Pred. No.: | 1.12e-71 | Length: | 994 | | | |
| Score: | 991.00 | Matches: | 193 | | | |
| Percent Similarity: | 99.5% | Conservative: | 0 | | | |
| Best Local Similarity: | 99.5% | Mismatches: | 1 | | | |
| Query Match: | 99.5% | Indels: | 0 | | | |
| DB: | 6 | Gaps: | 0 | | | |

US-08-817-997-2_COPY_36_229 (1-194) x AR050618 (1-994)

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Db 148 CAGCTGGAGCCTCGAGAACGGCTTGAGAGCGGAGCCCAACGCTCCCGCAGGCC 207
QY 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro 40
Db 208 ATCTGTATCTTTGCTCGCGCTCGACCGAGCGAGGCAACATGGGATCATCCGTCGCGCT 287
QY 41 AlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGly 60
Db 268 GCTCTCGCAACCGGCTTGAGTCCACATCCGGAACATCTGGATCCAGGCGCTCGCGGC 327
QY 61 ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
Db 328 CTTTACGAGCGCGCTGGCCACCACTTCTGCGCGGGGACCTCGGAGGCCAATC 387
QY 81 AspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal 100
Db 388 GACGAGGGCAAGCGCTGTTGGCTGGCCAAACCAAAAGTGCCCAACACGCGCTCGTC 447
QY 101 AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlnLeuSerGly 120
Db 448 GCCGGCGGTACAGCCAGGCGCGGCGCTCATGCTGCGCGCGCTCAGCGAGCTCAGCGGC 507
QY 121 AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
Db 508 GCCGTCAAGGACAGGTCAAGGCGCTGCGCTTTCGGATACCCCAAACTCCAGAAC 567
QY 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
Db 568 CTGGCGGCATCCCAACTACCGCGCGAGCGCACCAAGGTGTTCTGCAAGGTTGCGGAC 627
QY 161 AlaValCysThrGlyThrIleuIleThrProAlaHisIleuSerTyrThrIleGluAla 180
Db 628 GCCGTCTGACGCGGACGCTCATCATCACCGCGCGCATCTGTGTACAGCATCGAGGG 687
QY 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 688 CGCGGTGAGCGCGGAGGTCTCTGCGGGATCGCATCCGTCT 729
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RESULT 2

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LOCUS
DEFINITION Alternaria brassicicola cutinase (cutab1) gene, complete cds.
ACCESSION U03393

VERSION U03393.1 GI:416217

KEYWORDS

SOURCE Alternaria brassicicola

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.

REFERENCE 1 (bases 1 to 1545)

AUTHORS Yao, C. and Koeller, W.

TITLE Cloning and characterization of a cutinase gene from Alternaria

JOURNAL brassicicola

REFERENCE Physiol. Mol. Plant Pathol.

AUTHORS 2 (bases 1 to 1545)

Yao, C.

TITLE Direct Submission

JOURNAL Submitted (09-NOV-1993) Chenglin Yao, Plant Pathology, Cornell

University, Geneva, NY 14456, USA

LOCATION/Qualifiers

FEATURES

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688. .743
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774. .1235
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ORIGIN

Alignment Scores:
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Best Local Similarity: 54.5% Mismatches: 54
Query Match: 55.4% Indels: 22
DB: 15 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x ABU03393 (1-1545)

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QY 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMet----- 34
Db 646 ATCTTCATCTTCGCNAGGGGAGCAGCTGAAGCTGGAAACAT-GGTGAGTACAGCAATT 704
QY 35 -----GlyIleThrValGlyProAla 41
Db 705 CTCTACAGACTCTCCATAACAGCAATTAAACCATCACAGGGCGCACTCGTCGGTCCCTTC 764
QY 42 LeuAlaAsnGlyLeuGluSer-----HisIleArgAsnIleTrpIleGlnGlyValGly 59
Db 765 ACAGCAAAACCGCTCGAGAGCGCGTATGGGCGCATCCAAATGTTGGGTCCAGGGCGTAGT 824
QY 60 GlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsn 79
Db 825 GGCCCTATACCGCGCTCTCGTAGAGANTGCCCTTCCAGCGCGGTACTTCTCAAGCCGCC 884
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QY 100 ValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSer 119
Db 945 ACTGCCGCTGTACTCTCAAGGTGCTGCATGTCATGTCACACGCGATCCCGGCTCAGC 1004
QY 120 GlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGln 139
Db 1005 GCTGCCGTACAGACCAAAATCAAGGGGTGCTGTGTGTTTCGGGTACACTAAGAACTGCA 1064
QY 140 AsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGly 159
Db 1065 ANTGGAGGAGGATTCCAAACCTCCCTACAGCAGAGCAGCATCTACTGTGAACCCGG 1124
QY 160 AspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGlu 179
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RESULT 3
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LOCUS       A36991                718 bp    DNA    linear    PAT 05-MAR-1997
DEFINITION   Sequence 42 from Patent WO9403578.
ACCESSION    A36991
VERSION      A36991.1  GI:2294185
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unidentified
REFERENCE    1 (bases 1 to 718)
AUTHORS      Hijden,H.T., Marugg,J.D., Warr,J.F., Klugkist,J., Musters,W. and
              Hondmann,D.H.
TITLE        ENZYMATIC DETERGENT COMPOSITIONS
JOURNAL      Patent: WO 9403578-A 42 17-FEB-1994;
              UNILEVER PLC (GB)
COMMENT      Other publication CZ 9500242 951018
              Other publication CN 1088256 940622
              Other publication PL 307269 950515
              Other publication CA 2141559 940217
              Other publication AU 4700793 940303
              Other publication ZA 9305530 950130
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FEATURES     Location/Qualifiers
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Pred. No.:      1.36e-35      Length:      718
Score:          546.00      Matches:    108
Percent Similarity: 71.1%      Conservative: 32
Best Local Similarity: 54.8%      Mismatches: 53
Query Match:    54.8%      Indels:    4
DB:             6      Gaps:      3

US-08-817-997-2_COPY_36_229 (1-194) x A36991 (1-718)
QY      1 GlnLeuGly----AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
DB      103 CAGCTTGGTAGAACAACTCCGACGATCTGATCAACGGCAATAGCGCTTCCTCGCGCGAT 162
QY      20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
DB      163 GTCACTCTTCATTATGCTCAGAGTTCACAGAGACGGGCACTTGGGA---ACTCTCGGG 219
QY      40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
DB      220 CCAGCATTCCTCCCAACCTTGATTCGGCTTCGGCAAGGACGGTGTCTGATTCAGGGC 279
QY      58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
DB      280 GTTGGCGGTGCTTACCGAGCACCTTAGAGACAATGCTCTCCGCGGGGAACCTCTAGC 339
QY      78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
DB      340 GCCGCAATCAGGAGATGCTAGCGCTCTTCACAGAGCCCAACCAAGTCCCTCGACGCG 399
QY      98 ProValValAlaGlyTyrSerGlnGlyValAlaLeuIleAlaAlaValSerGlu 117
DB      400 ACTTTGATCGCGGTGGCTACACCGAGGCTGCTGACTTCAGCGCGGTAGCATCGAGGAC 459
QY      118 LeuSerGlyAlaValLysGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
DB      460 CTCGACTCGGCCATTCTGTGACAAGATCGCGGTACCGTTCTGTTTGGCTACCAACAAGAC 519
QY      138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
DB      520 CTACAGAAATCGCGCGGAATCCCAACTACCTCTCCGCGCAGGACCAAGGCTTCTCGCAAT 579
QY      158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177
DB      177
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Db      580 ACAGAGATCTCGTTTGTACTGTTGATGCTGTGCTGCACCTCCTTGGCATATGGT 639
QY      178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
DB      640 CCTGATGCCCGGACCTGCCCTCAGTTCTCATCGAGAGGTTCCGGGT 690

RESULT 4
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LOCUS       A39199                718 bp    DNA    linear    PAT 05-MAR-1997
DEFINITION   Sequence 47 from Patent WO9414963.
ACCESSION    A39199
VERSION      A39199.1  GI:2295568
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unidentified
REFERENCE    1 (bases 1 to 718)
AUTHORS      Egmond,M.R., Van,D.H., Musters,W., Peters,H., Verrips,C.T. and
              De,V.J.
TITLE        MODIFIED CUTINASES, DNA, VECTOR AND HOST
JOURNAL      Patent: WO 9414963-A 47 07-JUL-1994;
              UNILEVER PLC (GB)
COMMENT      Other publication SK 79595 951108
              Other publication PL 309388 951002
              Other publication CA 2150837 940707
              Other publication AU 5699994 940719
              Other publication CN 1090328 940803
              Other publication CZ 9501578 951213
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FEATURES     Location/Qualifiers
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Alignment Scores:
Pred. No.:      1.36e-35      Length:      718
Score:          546.00      Matches:    108
Percent Similarity: 71.1%      Conservative: 32
Best Local Similarity: 54.8%      Mismatches: 53
Query Match:    54.8%      Indels:    4
DB:             6      Gaps:      3

US-08-817-997-2_COPY_36_229 (1-194) x A39199 (1-718)
QY      1 GlnLeuGly----AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
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QY      20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
DB      163 GTCACTCTTCATTATGCTCAGAGTTCACAGAGACGGGCACTTGGGA---ACTCTCGGG 219
QY      40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
DB      220 CCAGCATTCCTCCCAACCTTGATTCGGCTTCGGCAAGGACGGTGTCTGATTCAGGGC 279
QY      58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
DB      280 GTTGGCGGTGCTTACCGAGCACCTTAGAGACAATGCTCTCCGCGGGGAACCTCTAGC 339
QY      78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
DB      340 GCCGCAATCAGGAGATGCTAGCGCTCTTCACAGAGCCCAACCAAGTCCCTCGACGCG 399
QY      98 ProValValAlaGlyTyrSerGlnGlyValAlaLeuIleAlaAlaValSerGlu 117
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QY      118 LeuSerGlyAlaValLysGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
DB      460 CTCGACTCGGCCATTCTGTGACAAGATCGCGGTACCGTTCTGTTTGGCTACCAACAAGAC 519
QY      138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
DB      520 CTACAGAAATCGCGCGGAATCCCAACTACCTCTCCGCGCAGGACCAAGGCTTCTCGCAAT 579
QY      158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177
DB      177
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Qy 20 AlaIleuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
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Qy 40 ProAlaIleuAlaAsnGlyLeuGlySerHisIle-----ArgAsnIleTrpIleGlnGly 57
Db 473 CTAGACATTCCTCCCAACCTTGAGTCCGCTTCGGCAAGACGGTGTCTGATTCAGGCG 532
Qy 58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db 533 GTTGGGGTGCCTACCGAGCCACTCTTGGAGACAATGCTCTCCCTCGCGAACCTCTAGC 592
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
Db 593 GCCCAATCAGGAGATGCTTGGTCTCTTCAGCAGGCCCAACACCAAGTGCCCTGAGCGG 652
Qy 98 ProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
Db 653 ACTTGTATCCCGGTGCTACAGCAGGGTCTGCATTCGACCGCGCTCCATCGAGGAC 712
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 713 CTCGACTCGGCCATTCTGTGACAGATCGCCGGAAGTCTTCTGTGGCTACACCAAGAC 772
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
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Db 893 CTTGATGCTCGTGGCCCTGCCCTGAGTCTCTCATCGAAGAGGTTCCGGCT 943
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RESULT 7

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LOCUS
DEFINITION F.solani pisi (fungus) cutinase mRNA, complete cds.
ACCESSION K02640
VERSION K02640.1 GI:168145
KEYWORDS cutinase; glycoprotein.
SOURCE Fusarium solani
ORGANISM Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
Soliday,C.L., Fluckey,W.H., Okita,T.W. and Kolattukudy,P.E.
Cloning and structure determination of cDNA for cutinase, an enzyme
involved in fungal penetration of plants
Proc. Natl. Acad. Sci. U.S.A. 81, 3939-3943 (1984)
Original source text: Fusarium solani pisi (strain T8) cDNA to
mRNA, clones C-[31,4,57].
[1] also sequenced a peptide isolated from a trypsin digest of
cutinase; the amino acid sequence as well as the initiation and
termination codons were used to identify the coding region of the
cDNA.
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The active serine catalytic triad and a disulfide bridge were located at bases 484 and 688, respectively. Disulfide bridges play an important role in maintaining catalytic activity. The presence of a single disulfide bridge and absence of any SH groups in the mature enzyme shows a discrepancy between this cutinase cDNA sequence and the chemical information concerning the mature enzyme.

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mRNA
CDS

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Score: 545.00 Matches: 108
Percent Similarity: 71.1% Conservative: 32
Best Local Similarity: 54.8% Mismatches: 53
Query Match: 54.7% Indels: 4
DB: 15 Gaps: 3
US-08-817-997-2_COPY_36_229 (1-194) x FSOCUT (1-883)
Qy 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db 166 CAGCTTGTAGAACAACTCGCAGCATCTGATCAACGGCAATAGCCCTTCTCCGCCGAT 225
Qy 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
Db 226 GTCATCTTCAITATGCCGAGGTTCAACAGAGACGGGCACTTGGGA---ACTCTCGGT 282
Qy 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
Db 283 CCTAGCATGTCTCCAACTTGAGTCCGCTTCGGCAAGACGGTCTCTGGATTCAAGGC 342
Qy 58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db 343 GTTGGCGGTGCTACCGAGCCACTCTTGGAGACAATGCTCTCCCTCGCGAACCTCTAGC 402
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
Db 403 GCCCAATCAGGAGATGCTCGGTCTCTTCCAGCAGGCCAACACCAAGTGCCCTGACGG 452
Qy 98 ProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
Db 463 ACTTTGATCGCGGTGGCTACAGCAGGGTGTCTGCATTCGACCGCCCTCCATCGAGGAC 522
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 523 CTCGACTCGGCCATTTCGTCAGACAGATCGCCGGAACCTGTTCTGTCGGCTACACCAAGAC 582
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
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Qy 158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db 643 ACAGGGGATCTCGTTTGTACTGTGATCTGATCTGTTGCTGACCTCCTTGGCTTATGGT 702
Qy 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 703 CTTGATGCTCGTGGCCCTGCCCTGAGTTCCTTCATCGAAGAGGTTCCGGCT 753
RESULT 8
COGCUA C-gloesporioides cutinase gene, complete cds.
LOCUS 1749 bp DNA linear PLN 27-APR-1993
DEFINITION
ACCESSION M21443
VERSION M21443.1 GI:167289
KEYWORDS cutinase.
SOURCE Glomerella cingulata
ORGANISM Glomerella cingulata
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes Incertae sedis; Phyllachorales; Phyllachoraceae;
Glomerella.

REFERENCE 1 (bases 1 to 1749)
AUTHORS Ettinger, W.F., Thukral, S.K. and Kolattukudy, P.E.
TITLE Structure of cutinase gene, cDNA, and the derived amino acid
sequence from phytopathogenic fungi
JOURNAL Biochemistry 26, 7883-7892 (1987)
COMMENT Original source text: C.gloeosporioides DNA (from papaya).
FEATURES
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ORIGIN 936 bp upstream of SacI site.

Alignment Scores:
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Score: 544.50 Matches: 110
Percent Similarity: 67.0% Conservative: 28
Best Local Similarity: 53.4% Mismatches: 48
Query Match: 54.7% Indels: 20
DB: 15 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x COGCUYA (1-1749)

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QY 27 GlySerThrGluProGlyAsnMet----- 34
Db 989 GCCTCGACTGAGCCCGGTAA CATGGTAAGGCTTCCTTCATCTTCAAAGCCCTATA 1048
QY 35 -----GlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSer-- 48
Db 1049 CTCACATTCGAAAGGAATCAGCGAGGCCCCCATCGTCGCCGAGCCCTGGAGAGAA 1108
QY 49 ----HisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAl 67
Db 1109 CTACGGCGCCACAAACGTCGTGGTCCAGGCGGTGGCGGCCCTTACCTGCCGACCTGGC 1168
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Db 1169 CTCCAACTTCCTGCCCGACGCGACCTCGTCGGGGGCCCATCAAGGAGGCCAGACGCTCTT 1228
QY 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnGl 107
Db 1229 CACCCTCGCCAAACACAAAGTGCCCAACGGCGCCATCGTCTGGGGCGGCTACAGCCAGG 1288
QY 107 yAlaAlaLeuIleAlaAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVally 127
Db 1289 CACGGCGGTGATGGGGCTTCATCTCAGGCTTGAGCACCAACGATCAAGAACACAGATCAA 1348
QY 127 sGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTy 147

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Db 2912 AACGAGCTCGAGACCGGACGAGCTCGCCTGCCCCAAGGTCATCTACATCTTTGCCCGT 2971
QY 27 GlySerThrGluProGlyAsnMet----- 34
Db 2972 GCCTCGACTGAGCGTGGTACATAGTGAAGGCTTCCTTCGGCCCATCTTCAAGGCCCATTA 3031
QY 35 -----GlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSer-- 48
Db 3032 TTGACATCTCGAATAGGATACGCGCAGGCCCATCTCGCCAGCCCTTAGAGAGAT 3091
QY 49 ----HisIleArgAsnIleThrIleGlnGlyValGlyGlyProIleAspAlaLeuAl 67
Db 3092 CTACGGTGCCAAACGAGCTGGGTTCAGGGCGTAGGGCGCCCTTACCTCGCGCACCTGGC 3151
QY 67 aThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPh 87
Db 3152 CTCCAACTCTCTGCCGACGGCACATCTCTGGCGGCCATCAACGAGGCGAGGCGCTTTT 3211
QY 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaIleGlyIleGlnGly 107
Db 3212 CACCTCTGCCCAACACAAAGTGCCTCCAAAGCGGCCATCTCTCGGGCGCTACAGCCAGG 3271
QY 107 yAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVally 127
Db 3272 CACCGCGCTGATCGCGGCTCCATCTCCGGCCTGAGCACCCAGCATCAAGAACCATCAA 3331
QY 127 sGlyValAlaLeuPheGlyIleThrGlnAnLeuGlnAsnArgGlyIleAlaLeu 147
Db 3332 GGGCGTGTGCTCTTCGGGTACACCAAGACCTGCAGAACCTGGCGCGCATCCCAACTT 3391
QY 147 rProArgGluArgLysValPheCysAsnValGlyAspAlaValCysThrGlyThrLe 167
Db 3392 CGAGAGCTCCAGACCGAGGTCTACTGGACATTCGGAGCGCGTCTGCTACGGCACCT 3451
QY 167 uIleIleThrProAlaHisLeuSerThrIleGluAlaArgGlyGluAlaAlaArgPh 187
Db 3452 GTTCATCTCTCGCGCGACCTTTTGTACAGACTGATGCGGCTGTTCGGCGCCCGCGATT 3511
QY 187 eLeuArgAspArgIle 192
Db 3512 CCTCCAGGCCCGCATT 3527
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RESULT 10
FSU63335
LOCUS Nectria ipomoeae cutinase (cutA) gene, complete cds.
DEFINITION Nectria ipomoeae cutinase (cutA) gene, complete cds.
ACCESSION U63335
VERSION U63335.1 GI:1488294
KEYWORDS
SOURCE Nectria ipomoeae
ORGANISM Nectria ipomoeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 3938)
AUTHORS Crowhurst,R.N., Binnie,S.J., Bowen,J.K., Hawthorne,B.T.,
Plummer,K.M., Rees-George,J., Rikkerink,E.H. and Templeton,M.D.
TITLE Effect of disruption of a cutinase gene (cutA) on virulence and
tissue specificity of Fusarium solani f. sp. cucurbitae race 2
toward Cucurbita maxima and C. moschata
Mol. Plant Microbe Interact. 10 (3), 355-368 (1997)
JOURNAL 9100380
PUBMED 2 (bases 1 to 3938)
REFERENCE Crowhurst,R.N.
AUTHORS Direct Submission
TITLE Submitted (09-JUL-1996) Plant Improvement Division, HortResearch,
JOURNAL 120 Mt Albert Rd., Auckland, New Zealand
FEATURES
source
location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 1,19e-33 Length: 3938
Score: 531.50 Matches: 109
Percent Similarity: 65.9% Conservative: 32
Best Local Similarity: 50.9% Mismatches: 52
Query Match: 53.4% Indels: 21
DB: 15 Gaps: 4
US-08-817-997-2_COPY_36_229 (1-194) x FSU63335 (1-3938)
QY 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db 2216 CAGCTTGGTAGAACAACTCGGACGATCTGATCAACGGCAACAGCGCTTCTCGCGCGAT 2275
QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMet----- 34
Db 2276 GTCATCTTCAATTATGCCGAGGTTCAACAGAGACGGGCAACTTGGTTCTAGAAATTGT 2335
QY 35 -----GlyIleThrValGlyProAlaLeu 42
Db 2336 TCTGATTACAACACCACCTTCTTACATACATATTAGGGA---ACACTCGGTCGAGCATC 2392
QY 43 AlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTirIleGlnGlyValGlyGly 60
Db 2393 GCCTCCAACTTGTAGTCCGCTTCGGAACGAGCGGTGTGATCCAGGCGGTGGCGT 2452
QY 61 ProIleAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
Db 2453 GCCTACCGAGCCACTCTTTGGGGACAACGCTCTGCCCGCGGAACCTCTAGCGCGGCATC 2512
QY 81 AspGlyGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal 100
Db 2513 CGGGAGATGCTCGGCTCTCTCCAGCAGGCCAACACCAAGTGCCTGACGCGACTCTGATC 2572
QY 101 AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGly 120
Db 2573 GCCGGTGTGTACAGCCAGGTCGTCATCTGCAGCGGCTCCATCGAGGACCTTGATCG 2632
QY 121 AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
Db 2633 GCTATTGCGCAGAGATCGCCGGAACCTGTTCTGTTTGGCTACACCAAGAACCTGCGAAG 2692
QY 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
Db 2693 CGTGCGCAATTCCTCCAACTACCTGCTGCAGGACCAAGGCTCTTCTGCAACGTTGGCGAT 2752
QY 161 AlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAla 180
Db 2753 CTCGTTTTCACCGGTAGCTTGTGCTGCTGCACTTCTGCGCTATGCTCTGATGCT 2812
QY 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 2813 CGTGCGCTCTCCCTGAGTTCCTTATCGAAGAGGTTTCGGCT 2854
RESULT 11
COGCTUB
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| | | | | | |
|--|--|--|------|--------|-----------------|
| LOCUS | COGCTUB | 2557 bp | DNA | linear | PLN 27-APR-1993 |
| DEFINITION | C.capsici cutinase gene, complete cds. | | | | |
| ACCESSION | M18033 | | | | |
| VERSION | M18033.1 | GI:167291 | | | |
| KEYWORDS | cutinase. | | | | |
| SOURCE | Colletotrichum capsici | | | | |
| ORGANISM | Colletotrichum capsici | | | | |
| REFERENCE | Ettenger,W.F., Thukral,S.K. and Kolattukudy,P.E. | | | | |
| AUTHORS | Structure of cutinase gene, cDNA, and the derived amino acid | | | | |
| TITLE | sequence from phytopathogenic fungi | | | | |
| JOURNAL | Biochemistry 26, 7883-7892 (1987) | | | | |
| COMMENT | Original source text: C.capsici DNA (from papaya). | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| | /number="1" | | | | |
| | /note="cutinase" | | | | |
| intron | 997..1053 | | | | |
| | /note="cut intron A" | | | | |
| exon | 1054..1542 | | | | |
| | /number="2" | | | | |
| ORIGIN | 5 bp upstream of PstI site. | | | | |
| Alignment Scores: | | | | | |
| Pred. No.: | 8.4e-34 | Length: | 2557 | | |
| Score: | 531.00 | Matches: | 108 | | |
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| DB: | 15 | Gaps: | 3 | | |
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| Qy | 7 | AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArg | 26 | | |
| Db | 913 | AACGAGCTTGAGTCTGGCAGCAGCTCCAACTGCCCAAGGTATCATCTTTGCTCGC | 972 | | |
| Qy | 27 | GlySerThrGluProGlyAsnMet | 34 | | |
| Db | 973 | GCCTCTACTGAGCCCGGTACATGGTAAGTCAGTCACAGCTCCCTTCACAGGAT | 1032 | | |
| Qy | 35 | -----GlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu | 47 | | |
| Db | 1033 | GATAACTGACTCTATATACAGGGCATCAGCGCAGGCCCACTTCGCCGACGCTTCGAA | 1092 | | |
| Qy | 48 | SerHis-----IleArganIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAla | 65 | | |
| Db | 1093 | AGCCGCTACGGCGCCTCACAGGCTCTGGGTCCAGGGCGTTGGCGGCCCTTACTCTGCGC | 1152 | | |
| Qy | 66 | LeuAlaThrAsnPhe---LeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLys | 84 | | |
| Db | 1153 | CTGGCTCCAACTTCATCATCCCGAGGGGACCTCCCGCGTCCGCACTCAACGAGGCTTAG | 1212 | | |
| Qy | 85 | ArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyr | 104 | | |

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Pred. No.: 4.86e-33 Length: 1735
Score: 519.50 Matches: 106
Percent Similarity: 65.2% Conservatives: 31
Best Local Similarity: 50.5% Mismatches: 55
Query Match: 52.2% Indels: 18
DB: 15 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x AF417004 (1-1735)

Qy 3 GlyAlaIleGluAenGlyLeuGluSerGlySerAlaAenAlaCysProAspAlaIleLeu 22
Db 504 GGAACACCCGCAACGATCTTACCAACGCAACAGCGCTTCTTGGCGCGATGTATCTTT 563
Qy 23 IlePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- 36
Db 564 ATCTATGCCGAGGTTCAACTGAGACGGCACTTGGTCCGTAGACTCTGTTCATATGGC 623
Qy 37 -----ThrValGlyProAlaLeuAlaAenGlyLeuG1 47
Db 624 AACATCACTCTCACATACACTAGGAACCTCTTGGCCCCAGCATCCGCTCCAAGCTCGA 683
Qy 47 uSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaA1 65
Db 684 GTCGGCTTCGGCAGGACGGCTCTGGATTCAAGGGGTTGGCGTCTACCGAGCCAC 743
Qy 65 aLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAenIleAspGluGlyLysAr 85
Db 744 TCTTGGAGACAATTCCCTCCCGCGGAACTCTAGCGCGCCATCATAGGAGATGCTCGG 803
Qy 85 gLeuPheAlaLeuAlaAenGlnLysCysProAsnThrProValValAlaGlyGlyTyrSe 105
Db 804 TCTCTTCCACGAGGCAACACCAAGTCCCGGACGCACTCTGATCCCGGTGGCTACAG 863
Qy 105 rGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluG1 125
Db 864 CCAAGGTGGCGACTTGGAGTCCCTCCGTCGAGGACCTCGACTCGGCCATCCGTGCAAA 923
Qy 125 nValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAl 145
Db 924 GATCGCGGGGACGGTCTGTGTCGTACTACTAGAACCTGCAGAACCCAGCGCCGATCCC 983
Qy 145 aAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrG1 165
Db 984 AAACCTTCCCTGCTGATAGAACCAAGGCTTCTGCAACACTGTGTATCTGTATGACAGG 1043
Qy 165 yThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaA1 185
Db 1044 TTCCTTGATCATGTCTGCGCCCTCACCTTACTTATGTCTGACGCTGTGCGCCAGCCCC 1103
Qy 185 aArgPheLeuArgAspArgIleArgAla 194
Db 1104 TGNATTCCTTATAGAAAGTTTCAGCT 1131

RESULT 13
FSOCUTA
LOCUS F.solani cutinase gene, complete cds.
DEFINITION M29759
ACCESSION M29759.1 GI:168147
KEYWORDS cutinase.
SOURCE Fusarium solani
ORGANISM Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 2769)
AUTHORS Soliday,C.L., Dickman,M.B. and Kolattukudy,P.E.
TITLE Structure of the cutinase gene and detection of promoter activity
in the 5'-flanking region by fungal transformation
JOURNAL J. Bacteriol. 171 (4), 1942-1951 (1989)
PUBMED 2703464
COMMENT Original source text: F.solani (f. sp. pisi (Nectria hematococa)
DNA.
FEATURES
Location/Qualifiers
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Db 1591 CTTTTGTACTGTAGTTCATCGTTCTCGCACTCACTTGGCTTATGGTCTCTGCTCG 1650
Qy 181 gglyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 1651 TGGCCCTGCCCTGAGTTCCTCATCGAAGAGGTTCGGGCT 1690

RESULT 14
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LOCUS
DEFINITION A.rabiei cut gene for cutinase.
ACCESSION X65628
VERSION X65628.1 GI:2472
KEYWORDS cut gene; cutinase.
SOURCE Mycosphaerella rabiei (anamorph: Ascochyta rabiei)
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothryiomycetes incertae sedis; Mycosphaerellaceae;
Mycosphaerella.
REFERENCE 1 (bases 1 to 1662)
Margolies-Clark,E., Tenkanen,M., Soderlund,H. and Penttila,M.
AUTHORS Acetyl xylan esterase from Trichoderma reesei contains an
TITLE active-site serine residue and a cellulose-binding domain
JOURNAL Eur. J. Biochem. 237 (3), 553-560 (1996)
PUBMED 8647098
REFERENCE 2 (bases 1 to 1662)
Tenhaken,R. and Barz,W.
AUTHORS Characterization and cloning of cutinase from ascochyta rabiei
TITLE Unpublished
JOURNAL
REFERENCE 3 (bases 1 to 1662)
Tenhaken,R.
AUTHORS Direct Submission
TITLE Submitted (21-APR-1992) R. Tenhaken, Institut fuer Biochemie und
JOURNAL Biotechnologie der Pflanzen, Hindenburgplatz 55, D-4400 Muenster,
FRG

FEATURES
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Location/Qualifiers
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ORIGIN
Alignment Scores: 5.61e-33 Length: 1662
Pred. No.: 518.50 Matches: 112
Score:

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Percent Similarity: 66.4% Conservative: 28
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DB: 15 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x ARCUT (1-1662)

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Db 612 ATCAGGTTCAGAACTCGAGAGGCGAGCGAGCTGTCCAAAGGCCATCTTAATTTT 671
Qy 25 AlaArgGlySerThrGluProGlyAsnMet----- 34
Db 672 GCCCGGGGACGACCGGAGATCGGCATATGATGTATGTCCTACTACCTGCACCCACCAC 731
Qy 35 -----GlyIleThrValGlyProAlaLeuAlaAn 44
Db 732 ACATGCACGCTTCTTAACACTTACACCGAGGGGTC-TCCGCGGGCGCGTGGCCAGC 790
Qy 45 GlyLeuGluSerHis----IleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAsp 63
Db 791 GCCCTCGAGGCTATGTGGCGCGACCAAAATCTGGGTCCAAAGCGCTCGCGGCCCTACACT 850
Qy 64 AlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGly 83
Db 851 GCAGATCTCCCTCCAACTTCTCGCGGGCGGCACCTCGCAATCGCCATCAACGAAGCG 910
Qy 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
Db 911 GTGGCGCTGTTCACGAAGCCACACCAATGCCCTCGACCCCATCGTGGCGCGCGC 970
Qy 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 971 TACAGCCAGGAAACGGCGCTCATGGCGGGCGCAATCCCAAACTCGAC---GCCGTGGC 1027
Qy 124 GluGlnValLysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGly 143
Db 1028 GCCAGGGTCTGGGCGCACGGTGCTGTTGGGTACAGCAGAACCCAGCAATACCAAGGGG 1087
Qy 144 IleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCys 163
Db 1088 ATCAAGATTACCCCGCAGAGGATCTGCAGGTGTATGTGAAGTGGCGATCTGTTTGT 1147
Qy 164 ThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGlu 183
Db 1148 GACGTTACGCTGATCATCACTGTGTGCACATTTTGTACTTGGAGGAGGCTCGCGGACG 1207
Qy 184 AlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 1208 GCGCGGAGTTTCTGAAGAGCAGATTTGGGCT 1240

RESULT 15
LOCUS
DEFINITION Nectria haematococca cutinase 3 (cut3) gene, complete cds.
ACCESSION AF417005
VERSION AF417005.1 GI:16417363
KEYWORDS
SOURCE Nectria haematococca (anamorph: Fusarium solani f. sp. pisi)
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 1697)
Li,D., Sirakova,T., Rogers,L., Ettiger,W.F. and Kolattukudy,P.E.
AUTHORS Regulation of constitutively expressed and induced cutinase genes
TITLE by different zinc finger transcription factors in Fusarium solani
f. sp. pisi (Nectria haematococca)
JOURNAL J. Biol. Chem. 277 (10), 7905-7912 (2002)
PUBMED 11756444
REFERENCE 2 (bases 1 to 1697)
Sirakova,T. and Kolattukudy,P.E.
AUTHORS Direct Submission
TITLE Submitted (05-SEP-2001) Neurobiotechnology Center, The Ohio State
JOURNAL

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University, 206 Rightmire Hall, 1060 Carmack Road, Columbus, OH

43210, USA

FEATURES

source

Location/Qualifiers

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/mol_type="genomic DNA"

/isolate="T8"

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join(405..599,649..1149)

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ORIGIN

Alignment Scores:

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| Query Match: | 52.0% | Indels: | 18 |
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US-08-817-997-2_COPY_36_229 (1-194) x AF417005 (1-1697)

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| Db | 504 | GGACACCCGCAACGATCTTACCAACGACGAGCGCTTCTGGCCGATGTAATCTTT | 563 |
| QY | 23 | IlePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- | 36 |
| Db | 564 | ATCTATGCCGAGTTCAACTGAGACGGGCAACTTGTGTCGTAGACTCTGTTCCAATGGC | 623 |
| QY | 37 | -----ThrValGlyProAlaLeuAlaAsnGlyLeuG | 47 |
| Db | 624 | AACATCACTCTCACATACACTAGGGAACCTCTTGGCCCCAGCATCGCTCCAAGCTCGA | 683 |
| QY | 47 | uSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAla | 65 |
| Db | 684 | GTCGGCTTCGGCAGGAGCGGCTCTGGATTAGGCGGTGGCGGTGCTTACCGAGCCAC | 743 |
| QY | 65 | aLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysar | 85 |
| Db | 744 | TCTTGAGACAATTCCTCCCGCGGAACCTCTAGCGCGGCATCAGGAGATGCTCG | 803 |
| QY | 85 | gLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSe | 105 |
| Db | 804 | TCTCTTCCAGCAGCCAAACCAAGTGCCTCGAGGACCTCTGATCGCGGTGGCTACAG | 863 |
| QY | 105 | rGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyValAlaValLysGlu | 125 |
| Db | 864 | CAAGGTGCGGCACCTTGCAGTGCCTCTCGTGGAGACCTCGACTCGGCCATCGTGACAA | 923 |
| QY | 125 | nValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAl | 145 |
| Db | 924 | GATCGCGGAGCGGTTCTGTTGGCTAGACTAGAACCTTGACAGAACACGCGCGATCCC | 983 |
| QY | 145 | aAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGl | 165 |
| Db | 984 | AAACTTCCTGCTGATAGAACCAAGGCTTCTTGTCAACACTGGTGATCTCGTATGCACAG | 1043 |

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|----|------|--|------|
| QY | 165 | yThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAl | 185 |
| Db | 1044 | TTCTTGATCATTCCTGCGCTCACCTTACTTATGCTCTGACGCTCGTGGCCGCCCC | 1103 |
| QY | 185 | aArgPheLeuArgAspArgIleArgAla | 194 |
| Db | 1104 | TGAGTTCTTATTGAGAAGGTTCCAGCT | 1131 |

Search completed: February 4, 2006, 23:14:33

Job time : 4853 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2006, 20:47:09 ; Search time 587 Seconds

(without alignments)
2202.641 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QGATENGLESANACPD.....SYTIARGEARFLDRIRA 194

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlh
-Q=/abes/ABSWEB_spool/US08817997/runat_03022006_161325_17986/app_query.fasta_1
-DB=N_Geneseq -QMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs04
-USER=us08817997 @CGN 1.1 727 @runat_03022006_161325_17986 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_21:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 996 | 100.0 | 1016 | 2 AAT29401 | Aat29401 Lipase co |
| 2 | 546 | 54.8 | 718 | 2 Aaq68591 | Aaq68591 Synthetic |
| 3 | 546 | 54.8 | 718 | 2 Aaq57027 | Aaq57027 Synthetic |
| 4 | 546 | 54.8 | 718 | 2 Aaq68583 | Aaq68583 Synthetic |

| | | | | | |
|----|-------|------|--------|---------------|--------------------|
| 5 | 546 | 54.8 | 1121 | 2 Aaq05859 | Cutinase |
| 6 | 519.5 | 52.2 | 2769 | 12 ADH34524 | Adh34524 Fucarium |
| 7 | 506 | 50.8 | 789 | 12 ADL27534 | Adl27534 cDNA sequ |
| 8 | 500.5 | 50.3 | 914 | 2 Aat95844 | Aat95844 Gliocladi |
| 9 | 499.5 | 50.2 | 999 | 2 Aat95846 | Aat95846 Trichopha |
| 10 | 497.5 | 49.9 | 675 | 12 ADN89479 | Adn89479 A. oryzae |
| 11 | 482 | 48.4 | 869 | 2 Aat95845 | Aat95845 Verticill |
| 12 | 455.5 | 45.7 | 780 | 12 ADN89480 | Adn89480 A. oryzae |
| 13 | 430 | 43.2 | 2371 | 12 ADL27533 | Adl27533 Genomic s |
| 14 | 262 | 26.3 | 280 | 2 Aaq68590 | Aaq68590 Cassette |
| 15 | 262 | 26.3 | 280 | 2 Aaq68582 | Aaq68582 Cassette |
| 16 | 260 | 26.1 | 768 | 12 ADH47688 | Adh47688 DNA encod |
| 17 | 260 | 26.1 | 798 | 4 Aaf23513 | Aaf23513 DNA encod |
| 18 | 260 | 26.1 | 798 | 6 ABK53022 | Abk53022 Aspergill |
| 19 | 260 | 26.1 | 798 | 12 ADK70254 | Adk70254 Aspergill |
| 20 | 240 | 24.1 | 275 | 2 Aaq57026 | Aaq57026 pur7208, |
| 21 | 212 | 21.3 | 242 | 2 Aaq57025 | Aaq57025 pur7208, |
| 22 | 212 | 21.3 | 246 | 2 Aaq68589 | Aaq68589 Cassette |
| 23 | 212 | 21.3 | 246 | 2 Aaq68581 | Aaq68581 Cassette |
| 24 | 192 | 19.3 | 1025 | 8 ABX13438 | Abx13438 A. oryzae |
| 25 | 189.5 | 19.0 | 651 | 13 ADR96587 | Adr96587 M. tuberc |
| 26 | 189.5 | 19.0 | 654 | 2 AAX34071 | Aax34071 Mycobacte |
| 27 | 189.5 | 19.0 | 654 | 13 ADU16604 | Adu16604 M. tuberc |
| 28 | 189.5 | 19.0 | 654 | 14 AEB92000 | Aeb92000 DNA encod |
| 29 | 189.5 | 19.0 | 720 | 2 AAX34072 | Aax34072 Mycobacte |
| 30 | 189.5 | 19.0 | 720 | 13 ADU16606 | Adu16606 M. tuberc |
| 31 | 189.5 | 19.0 | 1054 | 2 AAV63919 | Aav63919 Mycobacte |
| 32 | 189.5 | 19.0 | 1054 | 2 AAX81005 | Aax81005 Nucleotid |
| 33 | 189.5 | 19.0 | 15239 | 2 AAT33536 | Aat33536 BCG delet |
| 34 | 189.5 | 19.0 | 110000 | 4 AAI99682_22 | Continuation (23 o |
| 35 | 189.5 | 19.0 | 110000 | 4 AAI99683_22 | Continuation (23 o |
| 36 | 188.5 | 18.9 | 1060 | 2 AAV63921 | Aav63921 Mycobacte |
| 37 | 188.5 | 18.9 | 1060 | 2 AAX81007 | Aax81007 Nucleotid |
| 38 | 188.5 | 18.9 | 110000 | 4 AAI99682_25 | Continuation (26 o |
| 39 | 188.5 | 18.9 | 110000 | 4 AAI99683_25 | Continuation (26 o |
| 40 | 178 | 17.9 | 800 | 2 AAV63926 | Aav63926 Mycobacte |
| 41 | 178 | 17.9 | 800 | 2 AAX81033 | Aax81033 Nucleotid |
| 42 | 178 | 17.9 | 110000 | 4 AAI99682_38 | Continuation (39 o |
| 43 | 178 | 17.9 | 110000 | 4 AAI99683_38 | Continuation (39 o |
| 44 | 168 | 16.9 | 110000 | 4 AAI99682_41 | Continuation (42 o |
| 45 | 168 | 16.9 | 110000 | 4 AAI99683_41 | Continuation (42 o |

ALIGNMENTS

RESULT 1
AAT29401
ID AAT29401 standard; DNA; 1016 BP.
AC AAT29401;
XX
DT 17-DEC-1996 (first entry)
XX
DE Lipase coding sequence.
XX
KW Lipase; detergent; dishwashing; laundry; short-chain lipid; ss.
XX
OS Humicola insolens.
XX
FT Key Location/Qualifiers
FT CDS 43..783
FT /tag= a
FT /note= "immature protein"
FT sig_peptide 43..147
FT mat_peptide 148..780
FT /tag= b
FT /tag= c
XX
XX WO9613580-A1.
XX
PD 09-MAY-1996.
XX
PF 26-OCT-1995; 95WO-DK000427.

26-OCT-1994; 94DK-00001240.
(NOVO) NOVO-NORDISK AS.
Sandal T, Kauppinen S, Kofod LV;
WPI; 1996-239493/24.
P-PSDB; AAR95051.
Isolated DNA encoding lipolytic enzyme - derived from Humicola insolens DSM1800, used partic. as detergent additive for laundry and dishwashing compns.
Claim 1; Page 51; 63pp; English.
The present sequence encodes an enzyme with lipolytic activity, derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of about 20-21 kDa, a pI in the range of 709, a pH optimum of about 8 and has a specificity towards short-chain lipid substrates. It can be used as a detergent additive, partic. in compns. for laundry washing or dishwashing

Sequence 1016 BP; 231 A; 319 C; 289 G; 177 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,11e-99 Length: 1016
Score: 996.00 Matches: 194
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x AAT29401 (1-1016)

| | | | |
|----|-----|--|-----|
| Qy | 1 | GlnLeuGlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAla | 20 |
| Db | 148 | CAGCTGGAGGCATCGAAGCGCCTTGAGAGCGGAGCGCCACCGCTGCCCGCAGCGC | 207 |
| Qy | 21 | IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro | 40 |
| Db | 208 | ATCTGTGATCTTTGCTTCGGCGCTCGACCGAGCAGCGCACATCGGCTACCTCGGCGCT | 267 |
| Qy | 41 | AlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGly | 60 |
| Db | 268 | GCTCTGCGCAACGGCTTTGAGTCCACATCGGAACATCTGGATCCAGGCGCTCGCGCGC | 327 |
| Qy | 61 | ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle | 80 |
| Db | 328 | CTTTACGACGCGCGCTGGCCACCAACTCTCTCGCGCGGCGGACCTCGCAGGCGCAACATC | 387 |
| Qy | 81 | AspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal | 100 |
| Db | 388 | GACGAGGCGAAGCGCTGTGTCGCTGGCCACCAACAAAGTGCCTCCACAGCGCTCGTCGTC | 447 |
| Qy | 101 | AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGly | 120 |
| Db | 448 | GCCGCGGGTACAGCCAGGCGCGCGCTCATCGCTGCCCGCTCAGCGAGCTCAGCGCGC | 507 |
| Qy | 121 | AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn | 140 |
| Db | 508 | GCCGTCGAAGGAGCAGGTCAAGGCGCTCGCCCTCTTCGGATACACCCCAAAACCTCCAGAAC | 557 |
| Qy | 141 | ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp | 160 |
| Db | 568 | CGTGGCGGCATCGCCCAACTACCCCGCGAGCGCACCAAGGTGTTCTGCAACGTGTGGCGAC | 627 |
| Qy | 161 | AlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAla | 180 |
| Db | 628 | GCCGTCTGCACCGGACGCTCATCATCACCCTGGCGGCATCTGTGTGTACAGATCGAGGCG | 687 |
| Qy | 181 | ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla | 194 |

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Db 163 GTCACTTCATTATGCTCGAGTTCACAGAGCGGGCACTTGGA---ACTCTCGG 219
Qy 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
Db 220 CCCAGCATGCTCCCAACCTTGAGTCCGCCCTCGGCAAGACGGTGTCTGGATTTCAGGCG 279
Qy 58 ValGlyGlyProTyrAspAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db 280 GTTGGCGGTGCCCTACCGAGCCACCTTAGGAGACATGCTCTCCGCGGGGAACCTCTAGC 339
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
Db 340 GCCGCATCAGGAGATGTAGGCTCTTCAGCAGGCCCAACCAAGTGCCTCGACGCG 399
Qy 98 ProValAlaGlyGlyTyrSerGlnGlyValAlaLeuIleAlaAlaValSerGlu 117
Db 400 ACTTTGATCGCGGTGGCTACAGCCAGGGTGTCTGCACTTCGACGCGGTAGCATCGAGGAC 459
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 460 CTCGACTCGGCCATTCGTGACAAAGATCGCGGTACCGTCTCTGTTCGGCTACCAAGAAC 519
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
Db 520 CTAACAAATCGCGCGGGAATCCCACTACCTCGCAGCAGGACCAAGGTCTTCTGCAAT 579
Qy 158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177
Db 580 ACAGGAGATCTCGTTGTACTGTAGTGTGATGCTGCTGCACCTCACTTGGCATATGGT 639
Qy 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 640 CCTGATGCCCGGGGACTGCGCCCTGAGTTCCTCATCGAGAAGGTTCGGGCT 690

RESULT 3
AAQ57027
ID AAQ57027 standard; DNA; 718 BP.
XX
AC AAQ57027;
XX
DT 25-MAR-2003 (revised)
DT 10-AUG-1994 (first entry)
XX
DE Synthetic F. solani pisi cutinase gene.
XX
KW Cassette 1; cassette 2; cassette 3; Fusarium solani pisi; cutinase; gene;
KW enzyme; enzymatic; detergent; composition; surfactant; anionic; nonionic;
KW lipolytic activity; wash cycle; wash process; automatic; washing machine;
KW tumble drier; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 16..708
FT /tag= a
FT /product= "Pre-pro-cutinase"
FT sig_peptide 16..62
FT /tag= b
FT /note= "Pre-sequence"
FT misc_feature 63..107
FT /tag= c
FT /note= "Pro-sequence"
FT mat_peptide 108..708
FT /tag= d
FT /note= "Mature cutinase"
XX
PN WO9403578-A1.
XX
PD 17-FEB-1994.
XX
PF 20-JUL-1993; 93WO-EP001923.
XX

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PR 31-JUL-1992; 92GB-00016387.
XX
PA (UNIL ) UNILEVER PLC.
FA (UNIL ) UNILEVER NV.
XX
PI Van Der Hijden HTWM, Marugg JD, Warr JF, Klugkist J, Musters W;
PI Hondmann DHA;
XX
XX WPI; 1994-065669/08.
DR P-PSDB; AAR46295.
XX
XX Enzyme-contg. detergent compns. - comprises anionic-nonionic surfactant
XX system, and a lipolytic enzyme pref. a fungal cutinase derived from F.
XX solani pisi.
XX
XX Disclosure; Fig 1D; 67pp; English.
XX
XX This sequence represents the full length synthetic Fusarium solani pisi
XX cutinase gene which was constructed using the sequences given in AAQ57024
XX -26 which represent cutinase cassettes 1-3. The full length cutinase gene
XX was used in the production of the cutinase enzyme for use in an enzymatic
XX detergent composition. The composition also comprises (by wt.) 0.1-50% of
XX a surfactant system comprising 0-95% of 1 or more anionic surfactants and
XX 5-100% of 1 or more nonionic surfactants. The composition exhibits a
XX substantial lipolytic activity during the main cycle of a wash process in
XX an automatic washing machine, and consequently produces lipolytic
XX activity when used to wash fabrics which have not been in contact with
XX the detergent product before. The composition is also especially suitable
XX for use in combination with a tumble drier. (Updated on 25-MAR-2003 to
XX correct FN field.)
XX
SQ Sequence 718 BP; 144 A; 223 C; 191 G; 160 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 2,2e-50 Length: 718
Score: 546.00 Matches: 108
Percent Similarity: 71.1% Conservative: 32
Best Local Similarity: 54.8% Mismatches: 53
Query Match: 54.8% Indels: 4
DB: 2 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x AAQ57027 (1-718)

Qy 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db 103 CAGCTTGGTAGACAACACTCGCGACGATCTGATCAACGCAATAGCGTCTCTGCGCGCAT 162
Qy 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
Db 163 GTCATCTTCATTATGCTCGAGGTTCAACAGAGACGGGCACTTGGGA---ACTCTCGGG 219
Qy 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
Db 220 CCCAGCATGCTCCCAACCTTGAGTCCGCCCTTCGCAAGGACGGTGTCTGGATTACGGGC 279
Qy 58 ValGlyGlyProTyrAspAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db 280 GTTGGCGGTGCTTACCGAGCCACCTTAGGAGACATGCTCTCCGCGGGGAACCTCTAGC 339
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
Db 340 GCCGCATCAGGAGATGTAGGCTCTTCAGCAGGCCCAACCAAGTGCCTCGACGCG 399
Qy 98 ProValAlaAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
Db 400 ACTTTGATCGCGGTGGCTACAGCAGGCTGTGCTGCTTGCAGCGCTAGCAGGAC 459
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 460 CTCGACTCGGCCATTCGTGACAAAGATCGCGGTACCGTCTCTGCTTACCAAGAAC 519
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157

```

Db 520 CTACAGATCGGGCGGAATCCCACTACCTGCCGACGAGCACCAGGTCTTCTGCAAT 579
 QY 158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
 Db 580 ACAGAGAGATCGTTGTGTAAGTCTGATGCTGTGCTGCACCTCATTGGCATATGGT 639
 QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
 Db 640 CCTGATGCCGGGACCTGCCCTGAGTTCTCTCATGAGAAAGGTTCCGGGT 690

RESULT 4
 AAQ05853
 ID AAQ05853 standard; DNA; 718 BP.
 XX
 AC AAQ05853;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-MAR-1995 (first entry)
 XX
 XX Synthetic gene encoding Fusarium solani pisi pre-pro cutinase.
 XX
 KW Synthetic gene; cutinase; cassette; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 16..63
 FT /tag= a
 FT /product= "pre-sequence"
 FT 64..108
 FT /tag= b
 FT /product= "pro-sequence"
 FT 109..708
 FT /tag= c
 XX
 XX MO9414963-Al.
 PN
 XX
 PD 07-JUL-1994.
 XX
 PF 09-DEC-1993; 93WO-BP003550.
 XX
 PR 18-DEC-1992; 92EP-00204025.
 XX
 XX (UNIL) UNILEVER PLC.
 XX (UNIL) UNILEVER NV.
 XX
 PI Egmond MR, Van Der Hijden HTWM, Musters W, Peters H, Verrips CT;
 PI De Vlieg J;
 XX
 XX WPI: 1994-234698/28.
 DR P-PSDB; AAR59796.
 XX
 XX Eukaryotic cutinase variants with improved lipolytic activity - useful in
 PT detergent compans., with modified amino acid compsn. to increase
 PT hydrophobicity.
 XX
 XX Example; Fig ID: 77pp; English.
 PS
 CC A synthetic gene encoding Fusarium solani pisi pre-pro-cutinase was
 CC performed by assembly of three separate cassettes starting from synthetic
 CC DNA oligos. The synthetic cutinase gene was assembled and yielded pUR7210
 CC which comprises an ORF encoding the complete pre-pro-cutinase of F.
 CC solani pisi. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 718 BP; 144 A; 223 C; 190 G; 161 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,2e-50 Length: 718
 Score: 546.00 Matches: 108
 Percent Similarity: 71.1% Conservative: 32
 Best Local Similarity: 54.8% Mismatches: 53
 Query Match: 54.8% Indels: 4
 DB: 2 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x AAQ05853 (1-718)
 QY 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
 Db 103 CAGCTTGTTATACAACTCGGACGATCTGATCAACGCGCAATAGCGTCTCTCGCCGAT 162
 QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
 Db 163 GTCATCTTCAATTTATGCTCGAGGTTCAACAGAGACGGGCAACTTGGGA---ACTCTCGG 219
 QY 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
 Db 220 CCAGCAATTCCTCCAACTTGAATCGCCTTCGCGCAAGGACGGTGTCTGGATTTCAGGCG 279
 QY 58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
 Db 280 GTTGGCGGTGCTTACCGAGCCACCTAGGAGACAATGCTCTCCGCGGGAACTCTAGC 339
 QY 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
 Db 340 GCCGCAATCAGGGAGATGCTAGGCTCTTCCAGCAGGCGCAACACCAAGTCCCTCAGCG 399
 QY 98 ProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
 Db 400 ACTTTGATCGCGGTGGCTACAGCAGGTGCTGCACCTTGCAGCGCTAGCATCGAGGAC 459
 QY 118 LeuSerGlyAlaValLysGluInValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
 Db 460 CTGACTCGGCCATTCTGCACAGATCGCGGTACCGTCTCTGTCGGCTACACCAAGAAC 519
 QY 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
 Db 520 CTACAGAATCGGCGCGAATCCCACTACCTCCGACGAGACCAAGGTCTTCTGCAAT 579
 QY 158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
 Db 580 ACAGGAGATCTCGTTTGTACTGTGATGATGCTGTGTCACCTCCTCATGAGAGGTTTCGGGCT 639
 QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
 Db 640 CTGATGCCGGGACCTGCCCTGAGTTCTCTCATGAGAAAGGTTTCGGGCT 690

RESULT 5
 AAQ05859
 ID AAQ05859 standard; cDNA; 1121 BP.
 XX
 AC AAQ05859;
 XX
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 10-JAN-1991 (first entry)
 XX
 XX Cutinase gene of Fusarium solani pisi.
 XX
 KW cutinase; bridging peptide; acidolysis; alcohololysis; ss.
 XX
 OS Fusarium solani; pisi.
 XX
 XX Key Location/Qualifiers
 FH CDS 269..962
 FT /tag= a
 FT /product= "cutinase"
 FT /note= "putative"
 FT 269..317
 FT /tag= b
 FT 317..361
 FT /tag= c
 FT /label= bridging sequence
 XX
 XX WO9009446-A.
 XX
 PD 23-AUG-1990.

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XX 17-FEB-1989; 89EP-00400462.
XX
PR 17-FEB-1989; 89EP-00400462.
XX
PA (PLAN-) PLANT GENETICS SYST.
XX
PI Degeus P;
XX
DR WPI; 1990-275135/36.
DR P-PSDB; AAR06610.
XX
PT Pure recombinant cutinase and derivs. - used for hydrolysing or
PT synthesising ester(s) or for alcoholysis or acidolysis.
XX
PS Disclosure; Fig 1; 52pp; English.
XX
CC The cDNA encoding cutinase from amino acid residues 32 to 320 is
CC especially favoured for the production of cutinase derivatives. It is
CC operably linked to a promoter such as Ptac and a termination sequence
CC ,e.g. from Phase fd. A bridging sequence links the truncated cutinase to
CC the promoter sequences. The bridging sequence is constructed from the
CC signal sequence naturally associated with F.solani cutinase. Prokaryotic
CC cells (e.g. E.coli) transformed with the recombinant vector can produce
CC pure cutinase having higher thermostability than known lipases. See also
CC AAR06628-R06629. (Updated on 25-MAR-2003 to correct PI field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 1121 BP; 236 A; 320 C; 295 G; 270 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,97e-50 Length: 1121
Score: 546.00 Matches: 108
Percent Similarity: 71.1% Conservative: 32
Best Local Similarity: 54.8% Mismatches: 53
Query Match: 54.8% Indels: 4
DB: 2 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x AAQ05859 (1-1121)
QY 1 GlnLeuGly----AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
DB 356 CAGCTTGGTAGAACAACTCCGACGATCTCATCAACGGCAATAGCGTCTCTCGGCCGAT 415
QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
DB 416 GTCATCTTCAATTTATGCCGAGGTTCAACAGACGGGCACTTGGGA---ACTTCGGT 472
QY 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleThrIleGlnGly 57
DB 473 CCTAGCATTTGCTTCCAACTTGTAGTCCGCTTCGGCAAGGACGGTGTCTGATTCAGGCG 532
QY 58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
DB 533 GTTGGCGGTGCTTACCAGGCACTCTTGGAGACAATGCTCTCCCTCGCGGAACCTCTAGC 592
QY 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
DB 593 GCCGCAATCAGGAGATGTTGTGTCTTCCAGCAGCCCAACACCAAGTCCCTCGAGCG 652
QY 98 ProValValAlaGlyTyrSerGlnGlyValAlaAlaLeuIleAlaAlaValSerGlu 117
DB 653 ACTTTGATCGCGTGGCTACAGCCAGGGTGTGCTGCTTGCAGCCGCTTCCATCGAGGAC 712
QY 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
DB 713 CTGACTCGGCCAATCGTGACAGATCGCGGAAGTGTCTGTCTGCTGCTACACCAAGAC 772
QY 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
DB 773 CTACAGAACCGTGGCGAATCCCACTACCTCCGCGACAGGACCAAGGCTTCTCGCAAT 832
QY 158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177

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Db 833 ACAGGGATCTCGTTGTACTGTAGTTCGTTGCTGCACCTCACTTGGCTTATGCT 892
QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
DB 893 CCTGATGCTCGTGGCCCTGCCCTGAGTTCCTCATCGAGAGAGTTCCGGGCT 943

RESULT 6
ADH34524
ID ADH34524 standard; DNA; 2769 BP.
XX
AC ADH34524;
XX
DT 11-MAR-2004 (first entry)
XX
DE Fusarium solani cutinase gene.
XX
KW Alkanethiol; reactant ligand; substrate; protein chip;
KW polypeptide immobilisation; enzyme activity; antibody detection;
KW cutinase; gene; ds.
XX
OS Fusarium solani.
XX
PN US2003119054-A1.
XX
PD 26-JUN-2003.
XX
PF 07-AUG-2001; 2001US-00923760.
XX
PR 07-AUG-2001; 2001US-00923760.
XX
PA (MRKS/) MRKSICH M.
PA (HODN/) HODNELAND C.
XX
PI Mrksich M, Hodneland C;
XX
DR WPI; 2004-080248/08.
XX
PT New alkanethiols substituted with a reactant ligand useful for
PT immobilizing polypeptides on gold surfaces, e.g. for determining enzyme
PT activity or detecting antibodies.
XX
PS Example 7; SEQ ID NO 5; 57pp; English.
XX
CC The present invention relates to alkanethiols substituted with a reactant
CC ligand. Also disclosed is a substrate comprising a surface and a
CC plurality of moieties on the surface. The moieties are of formula Surf-L-
CC Q-T where T comprises a reactant ligand, and Surf designates where the
CC moiety attaches to the surface. The substrate can be incorporated into a
CC protein chip comprising a substrate bearing the reaction product of a
CC reactant ligand and a fusion polypeptide comprising a capture polypeptide
CC corresponding to the reactant ligand. The alkanethiols of the invention
CC are useful for immobilising polypeptides on gold surfaces, e.g. for
CC determining enzyme (especially kinase or protease) activity or detecting
CC antibodies. The present sequence representing the Fusarium solani
CC cutinase gene is used in the examples of the present invention.
XX
SQ Sequence 2769 BP; 553 A; 745 C; 592 G; 679 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.08e-46 Length: 2769
Score: 519.50 Matches: 107
Percent Similarity: 65.4% Conservative: 33
Best Local Similarity: 50.0% Mismatches: 54
Query Match: 52.2% Indels: 20
DB: 12 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x ADH34524 (1-2769)
QY 1 GlnLeuGly----AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
DB 1051 CAGCTTGGTAGAACAACTCCGACGATCTGTATCAACGGCAATAGCGTCTCTCGGCCGAT 1110

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QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- 36
Db 1111 GTCATCTTCATTATCCCGAGGTTCAACAGACAGACGGCAACTTGGTTCGTGAATTTCT 1170
QY 37 -----ThrValGlyProAlaLeuAl 43
Db 1171 TCTCATGACACATCATCTTTCTTACACATCCATTAGGGAACCTCTCGGTCCTAGCATGC 1230
QY 43 aAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyPr 61
Db 1231 CTCACACCTTGTAGTCCGCTTCGCGCAAGGAGCGGTCTGGATTTCAGGGCGTTGGCGGTGC 1290
QY 61 oTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAs 81
Db 1291 CTACGCAGCCACTCTTGGAGACAATGCTCTCCCTCGCGGAACCTCTAGCGCCGCAATCAG 1350
QY 81 pGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAl 101
Db 1351 GGAGATGCTCGGTCTCTTCAGCAGGCCAACACCAAGTGCCTTGACCGGACTTTGATCGC 1410
QY 101 aGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAl 121
Db 1411 CGGTGCTACAGCCAGGTTCTGCACTTGCAGCGGCTCCATCGAGGACCTCGACTCGGC 1470
QY 121 aValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnAr 141
Db 1471 CATTCGTGACACAGATCGCCGAACTGTTCTGTTTCGGCTACACCAAGAACCTACAGAACCG 1530
QY 141 gGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAl 161
Db 1531 TGCGCGAATCCCACTACCTCCGACAGGACCAAGGTCTTCTGCAATACAGGGGATCT 1590
QY 161 aValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaAr 181
Db 1591 CGTTTGACTGGTGTGATGATGTTGCTGCACCTCACTTGGCTTATGGTCTGATGCTCG 1650
QY 181 gGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 1651 TGCGCCTGCCCTGAGTTCTCTCATCGAAGGTTTCGGGCT 1690

RESULT 7
ADL27534
ID ADL27534 standard; cDNA; 789 BP.
AC ADL27534;
XX
DT 20-MAY-2004 (first entry)
DE
XX cDNA sequence of lipolytic enzyme NBE045.
XX lipolytic enzyme; NBE028; NBE029; NBE030; NBE031; NBE032; NBE033; NBE034;
KW NBE036; NBE038; NBE039; NBE043; NBE045; NBE042; dough; fungal infection;
KW enzyme; ss; gene.
XX Aspergillus niger.
XX
PH Key Location/Qualifiers
CDS 1..789
FT /*tag= a
FT /product= "lipolytic enzyme NBE045"
XX
XX W02004018660-A2.
XX
XX 04-MAR-2004.
XX
XX 15-AUG-2003; 2003WO-EP009145.
XX
XX 19-AUG-2002; 2002EP-00102168.
XX 19-AUG-2002; 2002EP-00102169.
XX 19-AUG-2002; 2002EP-00102170.
XX 19-AUG-2002; 2002EP-00102171.
XX 19-AUG-2002; 2002EP-00102172.
XX 19-AUG-2002; 2002EP-00102173.

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PR 19-AUG-2002; 2002EP-00102174.
PR 19-AUG-2002; 2002EP-00102176.
PR 19-AUG-2002; 2002EP-00102178.
PR 19-AUG-2002; 2002EP-00102179.
PR 19-AUG-2002; 2002EP-00102181.
PR 19-AUG-2002; 2002EP-00102183.
XX (STAM ) DSM IP ASSETS BV.
XX
XX Albarg R, Folkers U, Fritz A, Gerhard B, Heinrich O;
XX Ilgenfritz H, Maier D, Spreafico F, Wagner C, Boer DL, Meima RB;
XX
XX WPI; 2004-226841/21.
XX P-PSDB; ADL27535.
XX
XX Novel lipolytic enzyme, useful for producing dough and/or baked product
XX of dough, and for diagnosis of fungal infections.
XX
XX Claim 7; Page 126-127; 134pp; English.
XX
XX The present sequence encodes a lipolytic enzyme. The specification
XX describes the following lipolytic enzymes: NBE028, NBE029, NBE030,
XX NBE031, NBE032, NBE033, NBE034, NBE036, NBE038, NBE039, NBE043, NBE045
XX and NBE042. The lipolytic enzymes are useful for producing dough. They
XX are also useful for diagnosis of fungal infections. The enzymes have high
XX specificity towards the substrate, are less antigenic, and produce less
XX undesirable side activities when used in industrial processes and further
XX provide higher yields and low production cost.
XX
XX Sequence 789 BP; 167 A; 220 C; 229 G; 173 T; 0 U; 0 Other;
SQ

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Alignment Scores:

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Pred. No.: 6.26e-46 Length: 789
Score: 506.00 Matches: 101
Percent Similarity: 69.1% Conservative: 33
Best Local Similarity: 52.1% Mismatches: 54
Query Match: 50.8% Indels: 6
DB: 12 Gaps: 3

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US-08-817-997-2_copy_36_229 (1-194) x ADL27534 (1-789)

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QY 3 GlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu 22
Db 109 GGCCTCTACAGCAACGAATCCAAACTCGGATCCGACAAAGTCGCCTGCAGGGTGTGCGCGGC 159
QY 23 IlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeu 42
Db 160 ATCTTTGCGAGGGGTCACTGAGCTTGGGAATATGGCACCCTGAATCGGCCCCCTCTC 219
QY 43 AlaAsnGlyLeuGluSerHisIleArgAsn-----IleTrpIleGlnGlyValGlyGly 60
Db 220 TGCACACACCTGAAATCCAAACTCGGATCCGACAAAGTCGCCTGCAGGGTGTGCGCGGC 279
QY 61 ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
Db 280 CAATACAGCGCGGACTCGTCAGAAATGCCCTGCCCAAGACACCGATCCGGGGAGTATC 339
QY 81 AspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal 100
Db 340 TCCCGCGGAGGAGCATGTTTCAGAGGCGGAATTCGAAAGTGTCCCAATACTAAGATTGTT 399
QY 101 AlaGlyGlyTyrSerGlnGlyValAlaLeuIleAlaAlaValSerGluLeuSerGly 120
Db 400 CGGGGTGTTATAGTCAAGGAAGCGCTGTGATTGACACGCGCGTGCACAACTCAGCACC 459
QY 121 AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
Db 460 ACCGTGAAAGACCAAGTGAAGGGTGTCTGCTCTTCGGGTTTCACGAGAAACGTGCAGGAT 519
QY 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
Db 520 CACGGCGAGATCCCTAATTTACCTAAGGATGACGTAAGGTTTATTTGTCCCGTGGCGCAT 579

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QY 161 AlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAla 180
Db 580 CTGCTCTGTGATGATACGTTGGTTGTTACGGCGATGCATCTGACGTATGCATGCATGCG 639

QY 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 640 ---GSGTATCGCGAGCTTTTGGCCGAGAGGTGCAGTCT 678

RESULT 8
AAT95844
ID AAT95844 standard; DNA; 914 BP.
XX AC AAT95844;
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 11-MAY-1998 (first entry)
XX XX
XX Gliocladium lipolytic enzyme DNA.
XX Lipolytic enzyme; lipase; alkalophilic enzyme; detergent; surfactant;
KW esterification; lipid hydrolysis; optical isomer resolution; ss.
XX OS Gliocladium.
XX FH Key Location/Qualifiers
FT CDS 21..716
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
FT /*note= "Claim 22"

XX WO9741212-A1.
XX 06-NOV-1997.
XX 22-APR-1997; 97WO-DK000179.
XX 25-APR-1996; 96DK-00000500.
XX 25-APR-1996; 96DK-00000501.
XX (NOVO) NOVO-NORDISK AS.
XX Hirayama S, Taira R, Borch K, Sandal T, Halkier T, Oxenboell KM;
PI Nielsen B;
XX WPI; 1997-549717/50.
DR P-PSDB; AAW38262.
XX Lipolytic enzymes useful as detergent additives at high pH - from
PT Gliocladium, Verticillium and Trichophaea genera, give good washing
PT performance and stability in detergent solutions.
XX Claim 22; Page 37-38; 71pp; English.

XX This DNA sequence from Gliocladium sp. isolate NN140631 includes a coding
CC region for a novel lipase (see AAW38262) that has lipolytic activity at
CC alkaline pH and which gives good washing performance and stability in
CC detergent solutions. The lipase DNA was isolated by cloning a cDNA
CC library from isolate NN140631 in a vector, transforming yeast cells, and
CC screening by expressed lipolytic activity for positive clones. The
CC isolated DNA can be used for recombinant production of the lipase,
CC especially the mature enzyme. The DNA is deposited in Escherichia coli
CC transformant DSM 10591. Claimed lipases (see also AAW38263 and AAW38264)
CC can be used as detergent additives (e.g. as non-dusting granulates,
CC stabilised liquids, slurries or protected enzymes) to remove lipid or
CC fatty stains, and included with a surfactant in enzymatic detergent
CC compositions (claimed) e.g. for laundry and dishwashing, especially at
CC high pH. They are also useful for interesterification, total hydrolysis
CC of fats and oils and optical isomer resolution. (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 914 BP; 238 A; 210 C; 226 G; 240 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.06e-45 Length: 914
Score: 500.50 Matches: 95
Percent Similarity: 67.9% Conservative: 34
Best Local Similarity: 50.0% Mismatches: 58
Query Match: 50.3% Indels: 3
DB: 2 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x AAT95844 (1-914)

QY 5 IleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePhe 24
Db 144 GTGGTGACGAGCTGCGCAATGGC---GGCAGCGGTGCGCCCAAGCCATTCTCATCTTT 200

QY 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
Db 201 GCTCAGGCACAATGGAGCTGGATAACATGGCTTATTGGTGGGCCAGCTCTTGCAGGT 260

QY 45 GlyLeuGluSerHisIle-----ArgAsnIleThrIleGlnGlyValGlyGlyProTyr 62
Db 261 GGCTTAGAGGGCATCTTGGGTTTCGAACAACCTCTGGGTTCAAGGGGTGGGTGGCCAATAT 320

QY 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82
Db 321 GCCGCCAACCTTGAGGGCAATCTATTTCAGATGGAAACCTCTCTAAAGCCATCCAGGAG 380

QY 83 GlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 102
Db 381 ATGCTTAGCCCTGCTCCCAATTGGCGGACACCAAGTCCCAAACTCTAAGATTGTTACAGG 440

QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlyLeuSerGlyAlaVal 122
Db 441 GGTATAGCCAAAGGTGCTGCACTGGTGGCGCTGCTATTTCGGGATGTCAGGCTTCCATT 500

QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db 501 CGACAAAAGATTGTGGGAACCGTACTCTTTGGGTATACTTAAACAAACACAGACGACGGA 560

QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db 561 CAGGTAGAAAACCTACTCAACTGATCGGCTCGGGTTTACTGTAACTCGGAGACTTGATT 620

QY 163 CysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db 621 TGTCAAGGACCTTGATTGTTCTACCCACCATCTTCTTATGGAGTCCAGCTGCTGCT 680

QY 183 GluAlaAlaArgPheLeuArgAspArgIle 192
Db 681 CCAGCTGCCCAAGTTCTCTGCCGACCAAGATC 710

RESULT 9
AAT95846
ID AAT95846 standard; DNA; 999 BP.
XX AC AAT95846;
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 11-MAY-1998 (first entry)
XX XX
XX Trichophaea saccata lipolytic enzyme DNA.
XX Lipolytic enzyme; lipase; alkalophilic enzyme; detergent; surfactant;
KW esterification; lipid hydrolysis; optical isomer resolution; ss.
XX OS Trichophaea saccata.
XX FH Key Location/Qualifiers
FT CDS 68..766
FT /*tag= a

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FT sig_peptide 68..160
FT FT /*tag= b
FT mat_peptide 161..763
FT FT /*tag= c
FT FT /note= "Claim 22"
XX
PN WO9741212-A1.
XX
PD 06-NOV-1997.
XX
XX 22-APR-1997; 97WO-DK000179.
XX
XX 25-APR-1996; 96DK-00000500.
PR 25-APR-1996; 96DK-00000501.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Hirayama S, Taira R, Borch K, Sandal T, Halkier T, Oxenboll KM;
PI Nielsen B;
XX
DR WPI; 1997-549717/50.
DR P-PSDB; AAW38264.
XX
XX Lipolytic enzymes useful as detergent additives at high pH - from
PT Gliocladium, Verticillium and Trichophaea genera, give good washing
PT performance and stability in detergent solutions.
XX
XX Claim 22; Page 43-45; 71pp; English.
XX
XX This DNA sequence from Trichophaea saccata CBS 804.70 includes a coding
CC region for a novel lipase (see AAW38264) that has lipolytic activity at
CC alkaline pH and which gives good washing performance and stability in
CC detergent solutions. The lipase DNA was isolated by cloning a cDNA
CC library from T. saccata in a vector, transforming yeast cells, and
CC screening by expressed lipolytic activity for positive clones. The
CC isolated DNA can be used for recombinant production of the lipase,
CC especially the mature enzyme. The DNA is deposited in Escherichia coli
CC transformant DSM 11298. Claimed lipases (see also AAW38262 and AAW38263)
CC can be used as detergent additives (e.g. as non-dusting granulates,
CC stabilised liquids, slurries or protected enzymes) to remove lipid or
CC fatty stains, and included with a surfactant in enzymatic detergent
CC compositions (claimed) e.g. for laundry and dishwashing, especially at
CC high pH. They are also useful for interesterification, total hydrolysis
CC of fats and oils and optical isomer resolution. (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 999 BP; 260 A; 241 C; 239 G; 259 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,44e-45 Length: 999
Score: 499.50 Matches: 96
Percent Similarity: 67.4% Conservative: 32
Best Local Similarity: 50.5% Mismatches: 59
Query Match: 50.2% Indels: 3
DB: 2 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x AAT95846 (1-999)
QY 5 IleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePhe 24
DB 191 GTGCGTGATGAACGGCAATGCG---GGCGGCGGTGCCAAGGCCATTCATCTTT 247
QY 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
DB 248 GCTAGAGGTACATGGAGCTGGGATACATGGCTTATTAGTCGGCGCCAGCTCTTGCAGGT 307
QY 45 GlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyr 62
DB 308 GGCTTAGAGCTATGCTGGGTCAATAATACCTCTGGGTCCAAGGTAGTGGCCATAT 367
QY 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82
DB 368 GCTGCCAATCTCGAGGCAATCTATTTCAGATGGACACCTCCCAAGCCATCCAGGAG 427

QY 83 GlyIysArgLeuPheAlaLeuAlaAsnGlnIysCysProAsnThrProValValAlaGly 102
DB 428 ATGCTTAGTCTCTCCCAATTAGCGGACACCAAGTGTCCAAACTCTAAGATTGTTCACAGGG 487
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
DB 488 GGGTATAGCAAGCGCTGCACCTGTAGCCCTCTATTTCGGAGCTCAAGCTTCCATT 547
QY 123 LysGluGlnValIysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
DB 548 CGACAAAAGATTGTAGGAACCTGTACTCTTTGGGTACACCAAAACAAACAGAAAGACGA 607
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
DB 608 CAGGTAGAAAACCTACTCAACTGATCGACTCGCGGTATTATTCACACCGCGGAGACTTGATT 667
QY 163 CysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
DB 668 TGTCAAGGGACCTTGTATTGTTCTCGCAGCGCATCTTCTTTACGGAGATCAGGCTGCTGCT 727
QY 183 GluAlaAlaArgPheLeuArgAspArgIle 192
DB 728 CCAGCAGCCCAAGTTCCTTGCACGACAGATC 757

RESULT 10
ADN89479
ID ADN89479 standard; DNA; 675 BP.
XX
XX AC ADN89479;
XX
XX 29-JUL-2004 (first entry)
XX
XX A. oryzae plastic-degradation enzyme gene SEQ ID NO:4.
XX
XX ds; gene; plastic; biosurfactant; alpha-amylase; plastic-degrading;
XX enzyme.
XX
XX Aspergillus oryzae.
XX
XX Key Location/Qualifiers
XX CDS 1..675 /*tag= a
XX FT /product= "plastic-degrading enzyme"
XX
XX WO2004038016-A1.
XX
XX 06-MAY-2004.
XX
XX 17-SEP-2003; 2003WO-JP011861.
XX
XX 23-OCT-2002; 2002JP-00308884.
PR 24-DEC-2002; 2002JP-00371246.
XX
XX (TOHO-) TOHOKU TECHNOARCH KK.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
XX Abe K, Gomi K, Yamagata Y, Hasegawa F, Maeda H, Nakajima T;
PI Machida M;
XX
XX WPI; 2004-411219/38.
DR P-PSDB; ADN89486.
XX
XX Degradation of (waste) plastics with microorganisms particularly
XX transformants in presence of biosurfactant, applicable in producing
XX useful substances like proteins, metabolites and biosurfactants.
XX
XX Claim 48; SEQ ID NO 4; 139pp; Japanese.
XX
XX The invention relates to a novel method for degrading a plastic in the
XX presence of a biosurfactant using recombinant microorganisms. The method
XX of the invention is useful for the degradation of (waste) plastics and
XX also applicable in producing useful substances simultaneously e.g.

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CC proteins, metabolites and biosurfactants particularly alpha-amylase. The
CC present sequence encodes an A. oryzae plastic-degrading enzyme of the
CC invention.

XX SQ Sequence 675 BP; 144 A; 210 C; 174 G; 147 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,39e-45 Length: 675
Score: 497.50 Matches: 104
Percent Similarity: 67.3% Conservative: 28
Best Local Similarity: 53.1% Mismatches: 57
Query Match: 49.9% Indels: 7
DB: 12 Gaps: 4

US-08-817-997-2_COPY_36_229 (1-194) x ADN89479 (1-675)

QY 1 GlnLeuGlyAlaIleGluAsnGlyLeuGluSerAlaAsnAlaCysProAspAla 20
DB 97 CAGCTCGGCTCT---TCCATGACCTTACCACGGT-----GCATGCAAGGATGTG 144
QY 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro 40
DB 145 ACCCTCATTTTGGCTCGAGGCTCCCGCAATGGCAACATGGCACTGTCTATCGGACCC 204
QY 41 AlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyVal 58
DB 205 CCTCTCTGCTGCTGAGCAAGCAAGCTGCGCAGCAAGCTGCTTCCCAAGGTGTG 264
QY 59 GlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAla 78
DB 265 GGTGGCTTGTACAGGAGGATGTGCAAAATGCTCTCCCTCAGAACACCGACCCCGGC 324
QY 79 AsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrPro 98
DB 325 GCTATCTCACCGCAAGTCGCTTTGAACAGCCAGCACCAAGTGCCTTACACCCAG 384
QY 99 ValValAlaGlyClyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeu 118
DB 385 ATCGTGGCGGTGATACAGTCAAGGTAGTGGCTCATCGACAAACGCGTCCCAACAATC 444
QY 119 SerGlyAlaValGlyGlnValLysGlyValAlaLeuPheClyTyrThrGlnAsnLeu 138
DB 445 TCGCGCGAAGTCAAGCAAGGTCAAGGGTGTGTTTCTTCGGCTTCACTCGTAACCTC 504
QY 139 GlnAsnArgGlyClyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnVal 158
DB 505 CAGGACAGGGTCAGATCCCACTACCCCAAGGACAATGTTAAGGTCTTTTGTGGCATG 564
QY 159 GlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIle 178
DB 565 GGAGATCTTGTCTGCGATGCGACGCTTATGTACCGCGCCCATTTGACATATACCAT 624
QY 179 GluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
DB 625 AATGGC---CCGAGGCTGCTCTTTCCTTTCCTTTCGTCGAAGGTTCAAGTCA 669

RESULT 11

AAT95845

ID AAT95845 standard; DNA; 869 BP.

XX AC

XX AAT95845;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 11-MAY-1998 (first entry)

XX Verticillium lipolytic enzyme DNA.

DE Lipolytic enzyme; lipase; alkalophilic enzyme; detergent; surfactant;
XW esterification; lipid hydrolysis; optical isomer resolution; ss.
XX Verticillium.

FT Key Location/Qualifiers
FT CDS 43..741
FT /*tag= a
FT sig_peptide 43..132
FT /*tag= b
FT mat_peptide 133..738
FT /*tag= c
FT /note= "Claim 22"

XX MO9741212-A1.

XX 06-NOV-1997.

XX 22-APR-1997; 97WO-DK000179.

XX 25-APR-1996; 96DK-00000500.

XX 25-APR-1996; 96DK-00000501.

XX (NOVO) NOVO-NORDISK AS.

XX Hirayama S, Taira R, Borch K, Sandal T, Halkier T, Oxenboll KM;

XX Nielsen B;

XX WPI; 1997-549717/50.

XX P-PSDB; AAW38263.

XX Lipolytic enzymes useful as detergent additives at high pH - from
PT Gliocladium, Verticillium and Trichophaea genera, give good washing
PT performance and stability in detergent solutions.
XX Claim 22; Page 41-42; 71pp; English.

XX This DNA sequence from Verticillium sp. CBS 830.95 includes a coding
CC region for a novel lipase (see AAW38263) that has lipolytic activity at
CC alkaline pH and which gives good washing performance and stability in
CC detergent solutions. The lipase DNA was isolated by cloning a cDNA
CC library from the Verticillium sp. in a vector, transforming yeast cells,
CC and screening by expressed lipolytic activity for positive clones. The
CC isolated DNA can be used for recombinant production of the lipase,
CC especially the mature enzyme. The DNA is deposited in Escherichia coli
CC transformant DSM 10590. Claimed lipases (see also AAW38262 and AAW38264)
CC can be used as detergent additives (e.g. as non-dusting granulates,
CC stabilised liquids, slurries or protected enzymes) to remove lipid or
CC fatty stains, and included with a surfactant in enzymatic detergent
CC compositions (claimed) e.g. for laundry and dishwashing, especially at
CC high pH. They are also useful for interesterification, total hydrolysis
CC of fats and oils and optical isomer resolution. (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 869 BP; 235 A; 194 C; 204 G; 236 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.1e-43 Length: 869
Score: 482.00 Matches: 90
Percent Similarity: 68.0% Conservative: 33
Best Local Similarity: 49.7% Mismatches: 56
Query Match: 48.4% Indels: 2
DB: 2 Gaps: 1

US-08-817-997-2_COPY_36_229 (1-194) x AAT95845 (1-869)

QY 16 AlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGly 35
DB 196 GCTTGGCCCCAAGGTCCTCTCTTCTCGAGAACGATAGAACTTGATACATGGGC 255

QY 36 IleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIle 53
DB 256 TTATTGGTTGGGCCACCTTTTGCACGCTCTATCGGTATCTTGGTTCAAAAACCTC 315

QY 54 TrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAlaAlaThrAsnPheLeuProArg 73
DB 316 TGGGTCCCAAGCGTGGGTGGCCATATGCTCAAGCTTGGAGGGTAATCTCTTTCCGGAT 375

QY 74 GlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLys 93
 DB 376 GGGACCCCTCCTCAAGCCATCCAGGAGATGATTACATTCGTTCCAAATGGCGGATATAA 435
 QY 94 CysProAsnThrProValAlaAlaGlyGlyTyrSerGlnGlyAlaLeuIleAlaAla 113
 DB 436 TGTCCAACTCCAAAGATTGTCACTGGGGATATAGTCAGGTGCTGCTCTCGTGGCGCA 495
 QY 114 AlaValSerGluLeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGly 133
 DB 496 GCAATTCGGGATGTCAGGCTTCGATCCGACAGAGATTGTAGGAATGTACTGTTCCGG 555
 QY 134 TyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLys 153
 DB 556 TACTCCAAAACAAACAGAGAACGCGTCAGGTAGTAACTACTCTAATGACCGACTCCGA 615
 QY 154 ValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHis 173
 DB 616 GTTATTGCAACCTCGGGATTAAATTGGAGGGACCTTGATTGTTCTGCCAGTGCAC 675
 QY 174 LeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArg 193
 DB 676 CTCCTTTATGGAACCAAGCTTCTGCTGCTGCGACGACAAATTCCTCGTAGTAAATCAAT 735
 QY 194 Ala 194
 DB 736 TCT 738
 RESULT 12
 ADN89480
 ID ADN89480 standard; DNA; 780 BP.
 XX
 AC ADN89480;
 XX
 DT 29-JUL-2004 (first entry)
 DE
 DE A. oryzae plastic-degradation enzyme gene SEQ ID NO:5.
 KW ds; gene; plastic; biosurfactant; alpha-amylase; plastic-degrading;
 KW enzyme.
 XX
 OS Aspergillus oryzae.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..780
 FT /tag= a
 FT /product= "plastic-degrading enzyme"
 XX
 PN WO2004038016-A1.
 XX
 PD 06-MAY-2004.
 XX
 PF 17-SEP-2003; 2003WO-JP011861.
 XX
 PR 23-OCT-2002; 2002JP-00308884.
 PR 24-DEC-2002; 2002JP-00371246.
 XX
 PA (TORO-) TOHOKU TECHNOARCH KK.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Abe K, Gomi K, Yamagata Y, Hasegawa F, Maeda H, Nakajima T;
 PI Machida M;
 XX
 DR WPI; 2004-411219/38.
 DR P-PSDB; ADN89487.
 XX
 XX Degradation of (waste) plastics with microorganisms particularly
 PT transformants in presence of biosurfactant, applicable in producing
 PT useful substances like proteins, metabolites and biosurfactants.
 XX
 PS Claim 48; SEQ ID NO 5; 139pp; Japanese.
 XX
 CC The invention relates to a novel method for degrading a plastic in the

CC presence of a biosurfactant using recombinant microorganisms. The method
 CC of the invention is useful for the degradation of (waste) plastics and
 CC also applicable in producing useful substances simultaneously e.g.
 CC proteins, metabolites and biosurfactants particularly alpha-amylase. The
 CC present sequence encodes an A. oryzae plastic-degrading enzyme of the
 CC invention.
 XX
 SQ Sequence 780 BP; 164 A; 230 C; 197 G; 189 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,21e-40 Length: 780
 Score: 455.50 Matches: 95
 Percent Similarity: 65.1% Conservative: 28
 Best Local Similarity: 50.3% Mismatches: 61
 Query Match: 45.7% Indels: 5
 DB: 12 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x ADN89480 (1-780)

QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
 DB 88 AACGAGCTGCGAGATGGCTCT-----TSCAAGCGCATCACCTTCATCTTCCCGC 138
 QY 27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
 DB 139 GCTTCCACAGCCAGGACTTTTGGGTATATCACTGGCCCTGCGAGTCTGCAATGGCTTG 198
 QY 47 Glu---SerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAla 65
 DB 199 AAGATGCCAAAGCGGCCAAGTAGCTTGCAGGGGTGTGGACCCCAAGTACACGGCAGAC 258
 QY 66 LeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArg 85
 DB 259 CTGCGATCAAAATGCTTTGCCGAGAACACAGTCCCAGCTGCCATCCAAAGAGGCACAAGAC 318
 QY 86 LeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSer 105
 DB 319 CTGTTCCAGCAGCGCCGTCACCAAAATGCCCTCACACCCAAATTTGTGCCGGTGTATAGC 378
 QY 106 GlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGln 125
 DB 379 CAAGGCACAGCCGATGATGATGATCTCCATCAAGCGTCTACACAGACAACTGGAAGAGAG 438
 QY 126 ValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAla 145
 DB 439 ATCAAGGGTGTGCTGCTCTTCGGCTACACCCGACGACAGCAAGAACCGTCAAGTTGCC 498
 QY 146 AsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGly 165
 DB 499 AACTTTCCCAAGGACAAGGTCAAGGTCTACTGTGCCGTAGGCGATATGTTCTGTGACGGC 558
 QY 166 ThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAla 185
 DB 559 ACCTTGATCGTGGGGCCGCCCATTTCACTTAC---CTGGGTAACACCGCGAAGCAACT 615
 QY 186 ArgPheLeuArgAspArgIleArgAla 194
 DB 616 CAGTTCTTGTGTTGTAAGCTGAGTGCT 642

RESULT 13

ADL27533
 ID ADL27533 standard; DNA; 2371 BP.

XX
 AC ADL27533;

XX
 DT 20-MAY-2004 (first entry)

XX
 DE Genomic sequence of lipolytic enzyme NBE045.

XX
 KW lipolytic enzyme; NBE028; NBE029; NBE030; NBE031; NBE032; NBE033; NBE034;
 KW NBE036; NBE038; NBE043; NBE045; NBE046; dough; fungal infection;
 KW enzyme; ss.

OS *Aspergillus niger*.

XX WO2004018660-A2.

XX 04-MAR-2004.

XX 15-AUG-2003; 2003WO-EP009145.

XX 19-AUG-2002; 2002EP-00102168.

PR 19-AUG-2002; 2002EP-00102169.

PR 19-AUG-2002; 2002EP-00102170.

PR 19-AUG-2002; 2002EP-00102171.

PR 19-AUG-2002; 2002EP-00102172.

PR 19-AUG-2002; 2002EP-00102173.

PR 19-AUG-2002; 2002EP-00102174.

PR 19-AUG-2002; 2002EP-00102176.

PR 19-AUG-2002; 2002EP-00102178.

PR 19-AUG-2002; 2002EP-00102179.

PR 19-AUG-2002; 2002EP-00102181.

PR 19-AUG-2002; 2002EP-00102183.

XX (STAM) DSM IP ASSETS BV.

XX PA

XX PI Albarg R, Folkers U, Fritz A, Gerhard B, Heinrich O;

XX PI Ilgenfritz H, Maier D, Spreafico F, Wagner C, Boer DL, Meima RB;

XX XX WPI; 2004-226841/21.

XX PT Novel lipolytic enzyme, useful for producing dough and/or baked product

XX PT of dough, and for diagnosis of fungal infections.

XX PS Claim 7; Page 125-126; 134pp; English.

XX CC The present sequence encodes a lipolytic enzyme. The specification

CC describes the following lipolytic enzymes: NBE028, NBE029, NBE030,

CC NBE031, NBE032, NBE033, NBE034, NBE036, NBE038, NBE039, NBE043, NBE045

CC and NBE042. The lipolytic enzymes are useful for producing dough. They

CC are also useful for diagnosis of fungal infections. The enzymes have high

CC specificity towards the substrate, are less antigenic, and produce less

CC undesirable side activities when used in industrial processes and further

CC provide higher yields and low production cost.

XX SQ Sequence 2371 BP; 616 A; 587 C; 585 G; 583 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.13e-37 Length: 2371

Score: 430.00 Matches: 100

Percent Similarity: 51.0% Conservative: 33

Best Local Similarity: 38.3% Mismatches: 55

Query Match: 43.2% Indels: 74

DB: 12 Gaps: 5

US-08-817-997-2_COPY_36_229 (1-194) x ADL27533 (1-2371)

QY 3 GlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu 22

Db 1304 GGCTCTACAGCAACGAACTCGAGCAGGGAAGC-----TGCAAGATGTGACTCTC 1354

QY 23 IlePheAlaArgGlySerThrGluProGlyAsnMet----- 34

Db 1355 ATCTTTGCGAGGGGGTCAACTGAGCTTGGGAATATGTTGCTGCTTTTACC 1414

QY 34 ----- 34

Db 1415 CGTACTATCTATCTCCAGAACATACCAAGCACAACATCAAAACATGTGGAGCCAGGAG 1474

QY 35 -----GlyIleThrValGlyProAlaLeuAlaAsn 44

Db 1475 CTAATCAGTGGTGGTGTATGATGTAGGACACCGTAATCGGCCCTCTCTCGGAC 1534

QY 45 GlyLeuGluSerHisIleArgAsn-----IleTrpIleGlnGlyValGlyProTyr 62

Db 1535 AACCTGAATCCAAACTCGGATCCGAAAGAGTCCGTCGAGGGTGTGCGCGGCCAATAC 1594

QY 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82

Db 1595 AGCCCGGACTCGTGCAGATGCCCTGCCCAACACCGATCCCGGGAGTATCTCCGCC 1654

QY 83 GlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 102

Db 1655 GCGAAGCAGATGTTTCGAGGAGCGAATTCGAAGTGTCCCAATACTAAGATTGTTCGGGT 1714

QY 103 GlyTyrSer----- 105

Db 1715 GGTATATAG-GTATATATCCCTTTCCCTTTACCTTTCCCCCATATCAATGCTAGAGCAAA 1773

QY 106 -----GlnGlyAlaAlaLeuAlaAla 113

Db 1774 GGAATATCATGCTAATGTAGATGTTGGGAAACAGTCAAGGAAGCGCTGTGATTGACAAC 1833

QY 114 AlaValSerGluLeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGly 133

Db 1834 GCGGTGCAAGAACTCAGCACCCGCGTGAAGACCAAGTGAAGGGTGTGCTCTCTTCGGG 1893

QY 134 TyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLys 153

Db 1894 TTCACGAAACGTCGAGGATCACGGGCAGATCCCTAATTACCTTAAGGATGACGTGAAG 1953

QY 154 ValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHis 173

Db 1954 GTTTATTGTGCGTGGCGCATCTGCTCTGTGATGATACGTTGGTTGTACGCGCATGCAT 2013

QY 174 LeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArg 193

Db 2014 CTGACGTATGCGATGGATGCG---GGTGTGCGGCGAGCTTTTGGCCGGAAGGTGCAG 2070

QY 194 Ala 194

Db 2071 TCT 2073

RESULT 14

AAQ68590

ID AAQ68590 standard; DNA; 280 BP.

AC AAQ68590;

XX 25-MAR-2003 (revised)

DT 03-MAR-1995 (first entry)

XX Cassette 3 of synthetic Fusarium solani pisi cutinase gene.

DE Synthetic gene; cutinase; cassette; ds.

XX Synthetic.

PH Key Location/Qualifiers

FT misc_feature 1..43

FT /*tag= c

FT /label= oligo 3A

FT misc_difference 1..4

FT /*tag= a

FT /label= sticky end

FT complement(5'..34)

FT /*tag= i

FT /label= 3H

FT complement(35..79)

FT /*tag= j

FT /label= 3I

FT 44..88

FT /*tag= d

FT /label= 3B

FT complement(80..121)

FT /*tag= k

FT /label= 3J1

FT 89..130

FT /*tag= e

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2006, 21:53:49 ; Search time 3874 Seconds

(without alignments)
2342.977 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QGAIENGLESGSANACPD.....SYTIEARGEARFLRDIRA 194

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB_spool/US08817997/runat_03022006_161328_18041/app_query.fasta_1
-DB=EST -Qfmt=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs04
-USER=US08817997 @CGN 1.1 5315 @runat_03022006_161328_18041 -NCPU=6 -ICPU=3
-NO_MAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 564 | 56.6 | 775 | 8 | DR656248 |
| 2 | 564 | 56.6 | 790 | 8 | DR650105 |
| 3 | 564 | 56.6 | 812 | 8 | DR650176 |
| 4 | 564 | 56.6 | 864 | 8 | DR649823 |
| 5 | 564 | 56.6 | 873 | 8 | DR653698 |
| 6 | 564 | 56.6 | 873 | 8 | DR656249 |
| 7 | 564 | 56.6 | 874 | 8 | DR649822 |

8 564 56.6 874 8 DR653697
9 564 56.6 876 8 DR650104
10 564 56.6 880 8 DR648560
11 564 56.6 880 8 DR656090
12 564 56.6 881 8 DR650471
13 564 56.6 901 8 DR648561
14 564 56.6 905 8 DR650175
15 564 56.6 908 8 DR650470
16 564 56.6 913 8 DR656089
17 564 56.6 924 8 DR646042
18 564 56.6 924 8 DR655065
19 564 56.6 931 8 DR655066
20 511 51.3 672 8 DR646043
21 466 46.8 863 8 DR734519
22 447 44.9 766 6 CF391519
23 405 40.7 602 1 AJ638811
24 309.5 31.1 426 1 AI210810
25 301.5 30.3 479 1 AI210809
26 290.5 29.2 405 1 AI210575
27 284.5 26.6 603 3 BJ292902
28 262 26.3 736 7 CO139663
29 252 25.3 564 3 BM370193
30 241.5 24.2 419 1 AA787593
31 235.5 23.6 565 7 CO140029
32 232 23.3 868 6 CD645681
33 228.5 22.9 702 6 CA284076
34 218.5 21.9 467 6 CF391493
35 216.5 21.7 422 1 AA788247
36 196.5 19.7 704 8 CV950097
37 191 19.2 668 8 CV948750
38 188 18.9 665 8 CV957661
39 185.5 18.6 724 8 CV946800
40 179 18.0 814 7 CO200444
41 170 17.1 393 1 AA966137
42 159.5 16.0 720 7 CO218141
43 156 15.7 377 1 AI211957
44 155.5 15.6 585 8 CV953395
45 153.5 15.4 552 7 CO144719

ALIGNMENTS

RESULT 1

DR656248

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST1046365 FvN Gibberella moniliformis cDNA clone FVNB85, mRNA
775 bp linear EST 12-JUL-2005

sequence.

DR656248

DR656248.1 GI:70744724

EST.

Gibberella moniliformis

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 775)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Unterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonis gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAUR

USDA

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVNB85TH

Seq primer: AAT TAA CCC TCA AAG GG.

Location/Qualifiers

1..775

/organism="Gibberella moniliformis"

FEATURES
source


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/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVN8U85"
/tissue_type="mycelia"
/clone_lib="FVN"
/notes=vector: pbluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."

ORIGIN
Alignment Scores:
Pred. No.: 8.16e-55 Length: 775
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservat: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR656248 (1-775)
Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuPheAlaArg 26
Db 184 AATGATATGAGGATGGGATTCCTCCAGTTGTCCTCCAGCAATTCGATGCGCGT 243
Qy 27 GlySerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 244 GGTAGCAGACACTGGCACTTGGATCAGGTTGGGCGGATCCTCGCAGAGCCATG 303
Qy 47 GluSerHisLeuArgAsnLeuTrpIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db 304 CAGCTCGCTATCCAGACATCTGGATACAAAGTGTGGTGGGCGCTATAGCGCTGATCTC 363
Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnLeuAspGlyLeuArgLeu 86
Db 364 GCGCCCAACTTTCTCCGGAGGGGACTACTGATGCTCCATGATGAAGCTAAAGGCTG 423
Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db 424 TTCCAATGGCCCTACGATAGTGCCTCAGATACGCCGCTCGTACGGCTGTTATAGTCAA 483
Qy 107 GlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db 484 GGCAGGTTGCTGTCGGATATGCATCAGCGAACTTCAAAATCGCGCTCCAGAACCGATT 543
Qy 127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn 146
Db 544 GTTGGAGCTGCTGTTGGATATACCAAGACGAGCAGCTTGGGGCGCGTATTTCGGAAC 603
Qy 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db 604 TATCCTACGACAAACCAAGATCTTCTGCTCGCTACGATCTAGTGTGTGACGGAACT 663
Qy 167 LeuLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db 664 TTGTTCACTTCTGCTCATTTTCTATACGGTGACAGTGGCGGGTCCAGGTCGCGAA 723
Qy 187 PheLeuArgAspArgIle 192
Db 724 TTCTGTTGGACAGATT 741

RESULT 2
DR650105/c 790 bp mRNA linear EST 12-JUL-2005
LOCUS Gibberella moniliformis cDNA clone FVNAR36, mRNA
DEFINITION EST1040222 FVN Gibberella moniliformis cDNA clone FVNAR36, mRNA
sequence.
ACCESSION DR650105

VERSION DR650105.1 GI:70738581
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 790)
AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Uterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAUR
USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVNAR36TV
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/notes=vector: pbluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."
ORIGIN
Alignment Scores:
Pred. No.: 8.37e-55 Length: 790
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservat: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR650105 (1-790)
Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuPheAlaArg 26
Db 712 AATGATATGAGGATGGGATTCCTCCAGTTGTCCTCCAGCAATTCGATGCGCGT 653
Qy 27 GlySerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 652 GGTAGCAGACACTGGCACTTGGATCAGGTTGGGCGGATCCTCGCAGAGCCATG 593
Qy 47 GluSerHisLeuArgAsnLeuTrpIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db 592 CAGCTCGCTATCCAGACATCTGGATACAAAGTGTGGTGGGCGCTATAGCGCTGATCTC 533
Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnLeuAspGlyGlyLysArgLeu 86
Db 532 GCGGCCCAACTTTCTCCGAGGGGACTACTGATGCTCCATGATGAAGCTAAAGGCTG 473
Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db 472 TTCCAATGGCCCTACGATAGTGCCTCAGATACGCCGCTCGTACGGCTGTTATAGTCAA 413
Qy 107 GlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126

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Db      412  GGACGGTGTGTCGGATATGCACTCAGCAACTTCAATCGCGTCCAGAACAGGTT 353
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Db      352  GTTGGAGTCGCTTGTTCGATATACCAAGAACGAGCAGCTTGGGGCGCGTATTCGCAAC 293
QY      147  TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      292  TATCTTACCGCAAAACCAAGATCTTCTGTCGCTACCGATCTAGTGTGTGACGAACT 233
QY      167  LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db      232  TTGTTCAATCTTCTGCTCTATTTCTATACGGTGCAGATCGCGGGTCCAGTCCGGAA 173
QY      187  PheLeuArgAspArgIle 192
Db      172  TTCCTGGTTGGACAGATT 155

```

RESULT 3

DR650176/c
LOCUS EST1040293 FvN Gibberella moniliformis cDNA clone FVNAR82, mRNA
DEFINITION

ACCESSION DR650176

VERSION DR650176.1 GI:70738652

KEYWORDS EST.

SOURCE Gibberella moniliformis

ORGANISM Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 812)

REFERENCE

AUTHORS

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

CONTACT: Brown, D.W.

USDA/ARS/NCAUR

1815 N. University St., Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVNAR82TV

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

Location/Qualifiers

1. 812

/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVNAR82"

/tissue_type="mycelia"

/clone_lib="FvN"

/note="Vector: pBlueScript II SK(+); XR: Site 1: EcoRI;

Site 2: XhoI; anamorph: Fusarium verticillioides. Library

FvN was obtained from RNA derived from a corn meal medium

culture of strain M-3125. These cultures were prepared by

inoculating an autoclaved mixture of 25 g corn meal and 5

ml distilled water with 5 ml of water containing 5 x 10⁶

conidia. The inoculated medium was mixed thoroughly,

distributed equally into two 100-mm plastic petri dishes,

and incubated at room temperature for four or six

days."

ORIGIN

Alignment Scores:

Pred. No.: 8,68e-55 Length: 812

Score: 564.00 Matches: 109

Percent Similarity: 71.0% Conservativeness: 23

Best Local Similarity: 58.6% Mismatches: 54

Query Match: 56.6% Indels: 0

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DB:      8      Gaps:      0
US-08-817-997-2_COPY_36_229 (1-194) x DR650176 (1-812)
QY      7  AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
Db      712  AATGATATTGAGGATGGGATTCTCCAGTTTGTCCCCAGCAATTTCTGATCTATGCGCT 653
QY      27  GlySerThrGluProGlyAsnMetGlyThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db      652  GGTAGCAGAACCTGGCACTTGGATCAGGTTGGCGGATCCTCGCAGAGGCATG 593
QY      47  GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaIle 66
Db      592  CAGTCGCTATCCAGACATCTGGATACAGGTGTGGGGCCCTATACGGCTGATCTC 533
QY      67  AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db      532  GCGCCCAACTTCTTCGGAGGGGACTACTGATGCTCCATGATGAAGCTAAAGGCTG 473
QY      87  PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db      472  TTCCAAATGGCCTACGATAAGTGCACGATACGCGCTCGTGACGGCTGGTTATAGTCAA 413
QY      107  GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db      412  GGCACGGTGTGTCGGATATGCACCTCAGCAACTTCAAAATCGCGCTCCAGAACCGGTT 353
QY      127  LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db      352  GTTGGAGCTGCTGTTGGATATACCAAGAACGAGCAGCTTGGGGCGGCTATTCGGAAC 293
QY      147  TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      292  TATCTTACCGCAAAACCAAGATCTTCTGTCGCTACCGATTTAGTGTGACGGAAC 233
QY      167  LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db      232  TTGTTCAATCTTCTGCTCTATTTCTATACGGTGCAGATCGCGGGTCCAGTCCGGAA 173
QY      187  PheLeuArgAspArgIle 192
Db      172  TTCCTGGTTGGACAGATT 155

```

RESULT 4

DR649823/c

LOCUS EST1039940 FvN Gibberella moniliformis cDNA clone FVNAP59, mRNA

DEFINITION

sequence.

ACCESSION DR649823

VERSION DR649823.1 GI:70738298

KEYWORDS EST.

SOURCE Gibberella moniliformis

ORGANISM Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 864)

REFERENCE

AUTHORS

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

CONTACT: Brown, D.W.

USDA/ARS/NCAUR

1815 N. University St., Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVNAP59TV

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

Location/Qualifiers

1. 812

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source
1. .864
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNAP59"
/tissue="mycelia"
/clone_lib="FVN"
/notes="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."

ORIGIN
Alignment Scores:
Pred. No.: 9,44e-55 Length: 864
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservativeness: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR649823 (1-864)
Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuPheAlaArg 26
Db AATGATATTGGAGTGGGATTCCTCCAGTTGTCCCGCAGCAATTCCTGATCGCGT 631
Qy 27 GlySerThrGluProGlyAsnMetGlyLeuValGlyProAlaLeuAlaAsnGlyLeu 46
Db GGTAGCAGACAACTGGCAACCTTGGAAATCAGCTTGGGCCCATCTCCGAGCGCATG 571
Qy 47 GluSerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db GAGTCGCTATCCAGACATCTGGATACAGAGTTGGTGGGCCCTATACGGCTGATCTC 511
Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db GCGCCCAACTTCTTCGGAGGGGAGCTACTGATGCTCCATTCGATGAAGCTAAAGGCTG 451
Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyLysSerGln 106
Db TTCCAAATGGCTTACGATAAGTGCAGATACCGCGTGTGACGGCTGGTTATAGTCAA 391
Qy 107 GlyAlaAlaLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db GGACCGGTTGCTCGGATATGCACTCAGCGAACTTCAATCGCTCCAGAACCGATT 331
Qy 127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db GTTGGAGCTGCTTGTGGATATACCAAGACGAGCAGCTTGGGGCGGTATTCGGAAC 271
Qy 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db TATCCTACGACAAACCAAGATCTTCTGCTGCTACGGATCTAGTGTGTGACGGAACT 211
Qy 167 LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db TTGTTCTATCTTCTCTATTTTCTATACGGTGCAGATGCGCGGGTCCAGTCCGGA 151
Qy 187 PheLeuArgAspArgIle 192
Db TTTCTGTTGGACAGATT 133

RESULT 5
DR653698/c
LOCUS
DEFINITION
EST1043815 FVN Gibberella moniliformis cDNA clone FVNBE45. mRNA
873 bp mRNA linear EST 12-JUL-2005
sequence.
DR653698 1 GI:70742174
EST.
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 873)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.
Uterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendrick,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
USDA
1815 N. University St., Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brownw@ncaur.usda.gov
TIGR sequence name: FVNBE45TV
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES
Location/Qualifiers
1..873
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNBE45"
/tissue_type="mycelia"
/clone_lib="FVN"
/notes="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."
ORIGIN
Alignment Scores:
Pred. No.: 9,57e-55 Length: 873
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservativeness: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR653698 (1-873)
Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuPheAlaArg 26
Db AATGATATTGGAGTGGGATTCCTCCAGTTGTCCCGCAGCAATTCCTGATCTATGCGCGT 631
Qy 27 GlySerThrGluProGlyAsnMetGlyLeuValGlyProAlaLeuAlaAsnGlyLeu 46
Db GGTAGCAGACAACTGGCAACCTTGGAAATCAGCTTGGGCCCATCTCCGAGCGCATG 571
Qy 47 GluSerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db GAGTCGCTATCCAGACATCTGGATACAGAGTTGGTGGGCCCTATACGGCTGATCTC 511
Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db GCGCCCAACTTCTTCGGAGGGGAGCTACTGATGCTCCATTCGATGAAGCTAAAGGCTG 451
Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyLysSerGln 106
Db TTCCAAATGGCTTACGATAAGTGCAGATACCGCGTGTGACGGCTGGTTATAGTCAA 391
Qy 107 GlyAlaAlaLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db GGACCGGTTGCTCGGATATGCACTCAGCGAACTTCAATCGCTCCAGAACCGATT 331
Qy 127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db GTTGGAGCTGCTTGTGGATATACCAAGACGAGCAGCTTGGGGCGGTATTCGGAAC 271
Qy 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db TATCCTACGACAAACCAAGATCTTCTGCTGCTACGGATCTAGTGTGTGACGGAACT 211
Qy 167 LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db TTGTTCTATCTTCTCTATTTTCTATACGGTGCAGATGCGCGGGTCCAGTCCGGA 151
Qy 187 PheLeuArgAspArgIle 192
Db TTTCTGTTGGACAGATT 133

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RESULT 5

DR653698/C

STUDY

DEFINITION

DEF INE

| | | |
|---------------------|----------|------------------|
| Alignment Scores: | | |
| Pred. No.: | 9.57e-55 | Length: 873 |
| Score: | 564.00 | Matches: 109 |
| Percent Similarity: | 71.0% | Conservative: 23 |

USDA
1815 N. University St., Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brownid@ncaur.usda.gov
TIGR sequence name: FVNAP597H

```

LOCUS       DR653697               874 bp    mRNA    linear    EST 12-JUL-2005
DEFINITION   EST1043814 FvN Gibberella moniliformis cDNA clone FVNBE45, mRNA
sequence.
ACCESSION   DR653697
VERSION     DR653697.1
KEYWORDS    GI:70742173
SOURCE      Gibberella moniliformis
ORGANISM    Gibberella moniliformis
REFERENCE   1 (bases 1 to 874)
AUTHORS     Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,
            Uterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
            Kendra, D.F., Town, C.D. and Whitelaw, C.A.
TITLE       Analysis of 87,000 expressed sequence tags reveals alternatively
            spliced introns in multiple genes of the fumonisin gene cluster
            Unpublished (2005)
JOURNAL     Unpublished (2005)
COMMENT     Contact: Brown, D.W.
            USDA/ARS/NCAR
            USDA
            1815 N. University St, Peoria, IL 61604, USA
            Tel: 309 681 6230
            Fax: 309 681 6689
            Email: brown@ncar.usda.gov
            TIGR sequence name: FVNBE45TH
            Seq primer: AAT TAA CCC TCA CTA AAG GG.
            Location/Qualifiers
                source
                1..874
                /organism="Gibberella moniliformis"
                /mol_type="mRNA"
                /strain="m3125"
                /db_xref="taxon:117187"
                /clone="FVNBE45"
                /tissue_type="mycelia"
                /clone_lib="FvN"
                /notes="Vector: pBlueScript II SK(+); XR; Site 1: EcoRI;
                Site 2: XhoI; anamorph: Fusarium verticillioides. Library
                FvN was obtained from RNA derived from a corn meal medium
                culture of strain M-3125. These cultures were prepared by
                inoculating an autoclaved mixture of 25 g corn meal and 5
                ml distilled water with 5 ml of water containing 5 x 106
                conidia. The inoculated medium was mixed thoroughly,
                distributed equally into two 100-mm plastic petri dishes,
                and incubated at room temperature for four or six days."

ORIGIN
Alignment Scores:
Pred. No.: 9.58e-55 Length: 874
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservative: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR649822 (1-874)
QY 7 AsnglyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
Db 184 AATGATATTGAGGATGGGATTCCTCCAGTTGTCCCCAGCAATTCTGATCTATGCGGT 243
QY 27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 244 GGTAGCAGACACTGGCAACCTTGAATCAGCGTTGGCGCGATCCTCGCAGAGGCCATG 303
QY 47 GluSerHisIleArgAsnIleTrrIleGlnGlyValGlyProTyrAspAlaLeu 66
Db 304 CAGCTCGCTATCCAGACATCTGGATCAAGGTGTGGTGGCGCCCTATACGGCTGATCTC 363
QY 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db 364 GGGCCCAACTTCTTCGGGAGGGGATCTAGTGCCTCCATTGATGAGCTAAAGGCTG 423
QY 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db 424 TTCCAATGGCTTACGATAAGTCCAGATACGCCCGTGTGACGGCTGGTTATAGTCAA 483
QY 107 GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db 484 GGCACGGTTGTCTCGATATGACATCAGCAACTTCAATCCGCCGCTCAGAACCCAGGTT 543
QY 127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db 544 GTTGGAGCTGCCCTTGTGGATATACAGAACGAGCAGCTTGGGGGCGGTATTCGAA 603
QY 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db 604 TATCTTACGACAAACCAAGATCTTCTGTCTGCCATACCGATCTAGTGTGTGACGGA 663
QY 167 LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db 664 TTGTTCATTCTTCTGCTATTTCTATACGGTGCAGATCGCGGGTCCAGGTCCCGAA 723
QY 187 PheLeuArgAspArgIle 192
Db 724 TTCTCGTTGGACAGATT 741

RESULT 8
DR653697

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Db      424 TTCCAAATGGCTACGATAGTCCAGATACGCCGCTGCTGACGGCTGCTATAGTCAA 483
      QY      107 GlyAlaAlaLeuAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
      Db      484 GGCACCGTTGCTGCGGATATGCACTCAGCGAACTTCAATCGCCGCTCCAGAACCGAGTT 543
      QY      127 LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn 146
      Db      544 GTTGGAGCTGCTGTTGGATATACCAAGACGAGCAGCTTGGGGCGCTATTCGGAAC 603
      QY      147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
      Db      604 TATCTACGACAAACCAAGATCTTCTGTCTGCTACGATCTAGTGTGACGGAAT 663
      QY      167 LeuLeileThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
      Db      664 TTGTTATTCTTCTGCTCATTTCTATACGGTGCAGATCGCGGGTCCAGGTCCGGAA 723
      QY      187 PheLeuArgAspArgIle 192
      Db      724 TTCCTGGTTGGACAGATT 741

```

RESULT 9

```

DR650104      876 bp      mRNA      linear      EST 12-JUL-2005
LOCUS      EST1040221 FVN Gibberella moniliformis cDNA clone FVNAR36, mRNA
DEFINITION      sequence.

```

```

ACCESSION      DR650104
VERSION        DR650104.1 GI:70738580
KEYWORDS
SOURCE

```

```

ORGANISM

```

```

Gibberella moniliformis

```

```

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

```

```

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

```

```

1 (bases 1 to 876)

```

```

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

```

```

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

```

```

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

```

```

Analysis of 87,000 expressed sequence tags reveals alternatively

```

```

spliced introns in multiple genes of the fumonisin gene cluster

```

```

Unpublished (2005)

```

```

Contact: Brown, D.W.

```

```

USDA/ARS/NCAUR

```

```

1815 N. University St., Peoria, IL 61604, USA

```

```

Tel: 309 681 6230

```

```

Fax: 309 681 6689

```

```

Email: brown@ncaur.usda.gov

```

```

TIGR sequence name: FVNAR36TH

```

```

Seq primer: AAT TAA CCC TCA AAG GG.

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```

Location/Qualifiers

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```

1..876

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/organism="Gibberella moniliformis"

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/mol_type="mRNA"

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/strain="m3125"

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```

/db_xref="taxon:117187"

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/clone="FVNAR36"

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/tissue_type="mycelia"

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/clone_lib="FVN"

```

```

/notes="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;

```

```

Site 2: XhoI; anamorph: Fusarium verticillioides. Library

```

```

FVN was obtained from RNA derived from a corn meal medium

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culture of strain M-3125. These cultures were prepared by

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inoculating an autoclaved mixture of 25 g corn meal and 5

```

```

ml distilled water with 5 ml of water containing 5 x 106

```

```

conidia. The inoculated medium was mixed thoroughly,

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```

distributed equally into two 100-mm plastic petri dishes,

```

```

and incubated at room temperature for four or six days."

```

ORIGIN

```

Alignment Scores:
Pred. No.:      9.61e-55      Length:      876

```

```

Score:      564.00      Matches:      109
Percent Similarity:      71.0%      Conservative:      23
Best Local Similarity:      58.6%      Mismatches:      54
Query Match:      56.6%      Indels:      0
DB:      8      Gaps:      0

```

```

US-08-817-997-2_copy_36_229 (1-194) x DR650104 (1-876)

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```

QY      7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
      Db      204 AATGATATTGAGGATGGGATTTCTCCAGTTGTGCCCCAGCAATTTCTGATCTATGCGCT 263
      QY      27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
      Db      264 GTTAGCAGACAGAACCTGGCACTTGGATACAGGTTGGGCGCATCTCGCAGAGCCATG 323
      QY      47 GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeu 66
      Db      324 CAGCTCGCTATCCAGACATCTGGATACAGGTGTGGTGGGCCCTATACGCTGATCTC 383
      QY      67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
      Db      384 GCGCCCAACTTCTTCGCGAGGGGACTACTGATGCTCCATTGATGAAGCTAAAAAGGCTG 443
      QY      87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
      Db      444 TTCCAATGGCTTACGATAGTGCACAGATACGCCCGCTCGTGCAGCGCTGGTTTATAGTCAA 503
      QY      107 GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
      Db      504 GGCACGGTTGCTGCGGATGATGCACTCAGCGAATTTCAAATCGCGCTCAGAACCGATT 563
      QY      127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
      Db      564 GTTGGAGCTGCTGTTGGATATACCAAGACGAGCAGCTTGGGGCGCTATTCCGAC 623
      QY      147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
      Db      624 TATCTACGCAAAAACCAAGATCTTCTGTCTGCTACGGATCTAGTGTGTGACGAACT 683
      QY      167 LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
      Db      684 TTGTTATTCTTCTGCTCATTTTCTATACGGTGCAGATCGCGGGTCCAGGTCCGGAA 743

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QY      187 PheLeuArgAspArgIle 192
      Db      744 TTCCTGGTTGGACAGATT 761

```

RESULT 10

```

DR648560

```

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LOCUS

```

```

DEFINITION

```

```

sequence.

```

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DR648560

```

```

VERSION

```

```

DR648560.1 GI:70737035

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KEYWORDS

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SOURCE

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ORGANISM

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Gibberella moniliformis

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Gibberella moniliformis

```

```

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

```

```

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

```

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1 (bases 1 to 880)

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```

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

```

```

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

```

```

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

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Analysis of 87,000 expressed sequence tags reveals alternatively

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```

spliced introns in multiple genes of the fumonisin gene cluster

```

```

Unpublished (2005)

```

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Contact: Brown, D.W.

```

```

USDA/ARS/NCAUR

```

```

1815 N. University St., Peoria, IL 61604, USA

```

```

Tel: 309 681 6230

```

```

Fax: 309 681 6689

```


Email: browndw@nceaur.usda.gov
TIGR sequence name: FVNAH48TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.

FEATURES

source

1..880
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNAH48"
/tissue_type="mycelia"
/clone_lib="FVN"

/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10⁶
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."

ORIGIN

Alignment Scores:
Pred. No.: 9.67e-55 Length: 880
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservative: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR648560 (1-880)

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QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleuIlePheAlaArg 26
DB 197 AATGATATTGAGATGGGATTCCTCAGTTGTCCCGCAGCAATCTGATCTATGGCGGT 256
QY 27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
DB 257 GGTAGCAGACAGACCTGGCAACCTTGGAATCAGCTTGGGCGGATCCTCGCAGAGCCATG 316
QY 47 GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyraAspAlaLeu 66
DB 317 CAGCTCGCTATCCACACATCTCGATACAGAGTGTGGTGGGCCCTATACGGCTGATCTC 376
QY 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
DB 377 GCGCCCAACTTCTTCCGAGGGGACTACTGATGCTCCATTGATGAAGCTAAAGGCTG 436
QY 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyraSerGln 106
DB 437 TTCCAAATGGCTTACGATAGTGCACAGATACGCCGCTCGTACGGCTGTTATAGTCAA 496
QY 107 GlyAlaLeuAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluInVal 126
DB 497 GGCAGGTTGTCTGTCGGATATGCACTCAGCGAACTTCAAATCGCCGCTCCAGAACCGATT 556
QY 127 LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
DB 557 GTTGGAGCTGCCTTGTGATATACCAAGACGAGCAGCTTGGGGCCGCTATTCCGAAAC 616
QY 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
DB 617 TATCTTACGAGCAAAACCAAGATCTTCTGTCTCGCTACGGATCTAGTGTGTGACGGAAT 676
QY 167 LeuIleIleThrProAlaHisLeuSerTyrrIleGluAlaArgGlyGluAlaAlaArg 186
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QY 187 PheLeuArgAspArgIle 192
DB 737 TTCCTGGTTGGACAGATT 754
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RESULT 11

DR656090/c

LOCUS

DEFINITION

sequence.

ACCESSION

DR656090

VERSION

DR656090.1

KEYWORDS

EST.

SOURCE

ORGANISM

Gibberella moniliformis

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 880)

Brown, D.W., Cheung, P., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kandra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAUR

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: browndw@nceaur.usda.gov

TIGR sequence name: FVNB82TV

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

Location/Qualifiers

1..880

/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVNB82"

/tissue_type="mycelia"

/clone_lib="FVN"

/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;

Site 2: XhoI; anamorph: Fusarium verticillioides. Library

FVN was obtained from RNA derived from a corn meal medium

culture of strain M-3125. These cultures were prepared by

inoculating an autoclaved mixture of 25 g corn meal and 5

ml distilled water with 5 ml of water containing 5 x 10⁶

conidia. The inoculated medium was mixed thoroughly,

distributed equally into two 100-mm plastic petri dishes,

and incubated at room temperature for four or six days."

ORIGIN

Alignment Scores:

Pred. No.: 9.67e-55 Length: 880
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservative: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR656090 (1-880)

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QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleuIlePheAlaArg 26
DB 712 AATGATATTGAGATGGGATTCCTCAGTTGTCCCGCAGCAATCTGATCTATGGCGGT 653
QY 27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
DB 652 GGTAGCAGACAGACCTGGCAACCTTGGAATCAGCTTGGGCGGATCCTCGCAGAGCCATG 593
QY 47 GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyraAspAlaLeu 66
DB 592 CAGCTCGCTATCCACACATCTCGATACAGAGTGTGGTGGGCCCTATACGGCTGATCTC 533
QY 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
DB 532 GCGCCCAACTTCTTCCGAGGGGACTACTGATGCTCCATTGATGAAGCTAAAGGCTG 473
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Db      378  GCCTCCAACTTTCTTCGGAGGGGACTACTGATGCTCCATTTGATGAAGTAAAGGCTG 437
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Db      438  TTCCAAATGGCTTACGATAGTCCAGATACGCCCTGCTGACGGCTGTTATAGTCAA 497
Qy      107  GlyAlaLeuLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db      498  GGACAGGTTGCTGCTGGATGATGCACTCAGCAACTTCCAAATCGCCGTCAGAACACAGGTT 557
Qy      127  LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn 146
Db      558  GTTGGAGCTGCTTGTGTTGATATACCAAGACGAGCGCTTGGGGCCGCTATTCGAAAC 617
Qy      147  TyrProArgGluThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      618  TATCTACGGACAAACCAAGACTCTTCTGCTGCTACGGATCTAGTGTGTGACGGAAC 677
Qy      167  LeuLeuLeuThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db      678  TTCTTCATTTCTCTGCTCATTTTCTATACGTCGTCAGATCGCGGGTCCAGGTCCGGAA 737
Qy      187  PheLeuArgAspArgile 192
Db      738  TTCTCTGGTTGGACAGATT 755

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RESULT 15

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DR650470
LOCUS      908 bp      mRNA      linear      EST 12-JUL-2005
DEFINITION Gibberella moniliformis cDNA clone FVNAT77, mRNA
sequence.

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ACCESSION  DR650470
VERSION    DR650470.1  GI:70738946
KEYWORDS   EST.
SOURCE     Gibberella moniliformis

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ORGANISM   Gibberella moniliformis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

```

REFERENCE

```

AUTHORS    Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
            Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
            Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE       Analysis of 87,000 expressed sequence tags reveals alternatively
            spliced introns in multiple genes of the fumonisin gene cluster
            Unpublished (2005)
JOURNAL     Contact: Brown, D.W.
COMMENT     USDA/ARS/NCAUR

```

```

USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVNAT77TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.

```

FEATURES

source

```

1..908
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNAT77"
/tissue_type="mycelia"
/clone_lib="FVN"

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/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."

```

ORIGIN

```

Alignment Scores:      1.01e-54      Length:      908
Pred. No.:            564.00      Matches:      109
Score:                71.0%      Conservative: 23
Percent Similarity:   58.6%      Mismatches:  54
Best Local Similarity: 56.6%      Indels:       0
Query Match:          8           Gaps:        0
DB:

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US-08-817-997-2_COPY_36_229 (1-194) x DR650470 (1-908)

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Qy      27  GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db      258  GGTAGCACAGAACCTGGCAACTTGGAAATCAGGTTGGGCCGATCTCCGAGAGGCCATG 317
Qy      47  GluSerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db      318  CAGTCGCTATCCAGACATCTGGATACAGGTGTGGTGGGCCCTATACGGCTGATCTC 377
Qy      67  AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db      378  GCGCCCAACTTTCTTCGGAGGGGACTACTGATGCTCCATTTGATGAAGCTAAAGGCTG 437
Qy      87  PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db      438  TTCCAAATGGCTTACGATAGTGGCCAGATACGCCCTGCTGACGGCTGTTATAGTCAA 497
Qy      107  GlyAlaLeuLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db      498  GGCACGGTTGCTGCTGGATATGCACTCAGCAACTTCCAAATCGCCGTCAGAACACAGGTT 557
Qy      127  LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn 146
Db      558  GTTGGAGCTGCTTGTGTTGATATACCAAGAACGAGCAGCTTGGGGCCGCTATTCGGAAC 617
Qy      147  TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      618  TATCTACGGACAAACCAAGACTCTTCTGCTGCTACGGATCTAGTGTGTGACGGAAC 677
Qy      167  LeuLeuLeuThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGlyGluAlaAlaArg 186
Db      678  TTGTTCATTTCTCTGCTCATTTTCTATACGTCAGATCGCGGGTCCAGGTCCGGAA 737
Qy      187  PheLeuArgAspArgile 192
Db      738  TTCTCTGGTTGGACAGATT 755

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Search completed: February 5, 2006, 00:19:11
Job time : 3878 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2006, 22:50:57 ; Search time 161 Seconds
(without alignments)
2141.907 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QUGATENGLESANACPDPA.....SYTIERGEARFLDRIRA 194

Scoring table:

| | |
|---------------------------|---------------------------|
| BLOSUM62 | Xgapop 10.0 , Xgapext 0.5 |
| Ygapop 10.0 , Ygapext 0.5 | |
| Fgapop 6.0 , Fgapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSWEB_spool/US08817997/runat_03022006_161330_18065/app_query.fasta_1
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abs06p -USER=US08817997 @CGN 1.1.290 @runat_03022006_161330_18065
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------|-------------------|
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| 2 | 500.5 | 50.3 | 914 | US-09-177-234-2 | Sequence 2, Appli |
| 3 | 499.5 | 50.2 | 999 | US-09-177-234-7 | Sequence 7, Appli |
| 4 | 482 | 48.4 | 869 | US-09-177-234-5 | Sequence 5, Appli |
| 5 | 260 | 26.1 | 768 | US-10-231-478-2 | Sequence 2, Appli |
| 6 | 260 | 26.1 | 798 | US-09-585-468-2 | Sequence 2, Appli |
| 7 | 260 | 26.1 | 798 | US-10-114-115A-2 | Sequence 2, Appli |
| 8 | 260 | 26.1 | 798 | US-10-114-116-2 | Sequence 2, Appli |
| 9 | 260 | 26.1 | 798 | US-09-999-170-1 | Sequence 1, Appli |

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| 10 | 189.5 | 19.0 | 651 | 3 | US-09-894-844-13 | Sequence 13, Appli |
| 11 | 189.5 | 19.0 | 1054 | 3 | US-09-050-739-9 | Sequence 9, Appli |
| 12 | 189.5 | 19.0 | 15239 | 2 | US-08-390-878-17 | Sequence 17, Appli |
| c 13 | 189.5 | 19.0 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| c 14 | 189.5 | 19.0 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| 15 | 188.5 | 18.9 | 1060 | 3 | US-09-050-739-13 | Sequence 13, Appli |
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| 17 | 188.5 | 18.9 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| 18 | 178 | 17.9 | 800 | 3 | US-09-050-739-51 | Sequence 51, Appli |
| 19 | 167.5 | 16.8 | 950 | 3 | US-09-050-739-55 | Sequence 55, Appli |
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| 23 | 130 | 13.1 | 1125 | 3 | US-09-324-542-153 | Sequence 153, App |
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| 25 | 120.5 | 12.1 | 470 | 3 | US-09-060-756-157 | Sequence 157, App |
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| 34 | 98 | 9.8 | 287 | 3 | US-09-533-559-1362 | Sequence 1362, Ap |
| c 35 | 97 | 9.7 | 11029 | 3 | US-09-902-540-1004 | Sequence 1004, Ap |
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| 37 | 91 | 9.1 | 420 | 3 | US-09-670-314-496 | Sequence 496, App |
| c 38 | 91 | 9.1 | 601 | 3 | US-09-949-016-181597 | Sequence 181597, |
| c 39 | 91 | 9.1 | 601 | 3 | US-09-949-016-181598 | Sequence 181598, |
| c 40 | 89.5 | 9.0 | 125672 | 3 | US-09-949-016-16956 | Sequence 16956, A |
| c 41 | 89.5 | 9.0 | 276687 | 3 | US-09-949-016-13840 | Sequence 13840, A |
| 42 | 88 | 8.8 | 2163 | 3 | US-09-252-991A-5310 | Sequence 5310, Ap |
| c 43 | 88 | 8.8 | 3282 | 3 | US-09-252-991A-5256 | Sequence 5256, Ap |
| c 44 | 88 | 8.8 | 4158 | 3 | US-09-252-991A-5348 | Sequence 5348, Ap |
| c 45 | 88 | 8.8 | 4953 | 3 | US-09-252-991A-5227 | Sequence 5227, Ap |

ALIGNMENTS

RESULT 1

US-08-817-997A-1
; Sequence 1, Application US/08817997A
; Patent No. 5827719
; GENERAL INFORMATION:
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Kofod, Lene V.
; TITLE OF INVENTION: An Enzyme With Lipolytic
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58277190 No. 5827719disk Of No. 5827719th America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,997A
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 7435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4316.204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 43..729
OTHER INFORMATION:
US-08-817-997A-1

Alignment Scores:
Pred. No.: 2,69e-105 Length: 994
Score: 991.00 Matches: 193
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 2 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x US-08-817-997A-1 (1-994)

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QY 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro 40
DB 208 ATCTGATCTTTCTCGCGCTCGAGCGAGCCAGGCAACATGGGCATCACCGTCGGCCCT 267
QY 41 AlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGly 60
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DB 328 CCTTACGAGCGCGCTGGCCACCACTTCTCGCGGGGCGCACCTCGCAGGGCAACATC 387
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DB 508 GCCGTCAAGGAGCAGGTCAAGGGGTGCGCTCTTCGATACACCCAAACCTCCAGAAC 567
QY 141 ArgGlyGlyIleAlaAsnTyProArgGluArgThrLysValPheCysAsnValGlyAsp 160
DB 568 CGTGGCGCATCCCACTACCGCGCAGCGACCAAGGTGTTCTGCAACGTTGGCGAC 627
QY 161 AlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyThrIleGluAla 180
DB 628 GCGGTCTGCACCGGCACGCTCATCATCACCCCGCGCATCTGTGTACATCATCGAGCG 687
QY 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
DB 688 CGCGGTGAGCCGGAGGTTCCTGCGGGATCGCATCCGTGCT 729

RESULT 2

US-09-177-234-2
Sequence 2, Application US/09177234A
Patent No. 6350604
GENERAL INFORMATION:
APPLICANT: Hirayama, Satoshi
APPLICANT: Taira, Rikako
APPLICANT: Borch, Kim
APPLICANT: Sandal, Thomas

APPLICANT: Halkier, Torben
APPLICANT: Oxendoll, Karen M.
APPLICANT: Nielsen, Bjarne R.
TITLE OF INVENTION: Alkaline Lipolytic Enzyme
FILE REFERENCE: 4698.204-US
CURRENT APPLICATION NUMBER: US/09/177,234A
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: 500/96
EARLIER FILING DATE: 1996-04-25
EARLIER APPLICATION NUMBER: 501/96
EARLIER FILING DATE: 1996-04-25
EARLIER APPLICATION NUMBER: PCT/DK97/00179
EARLIER FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 914
TYPE: DNA
ORGANISM: Gliocladium sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (21)...(713)
NAME/KEY: mat_peptide
LOCATION: (114)...(713)
NAME/KEY: sig_peptide
LOCATION: (21)...(113)
US-09-177-234-2

Alignment Scores:
Pred. No.: 1,62e-48 Length: 914
Score: 500.50 Matches: 95
Percent Similarity: 67.9% Conservative: 34
Best Local Similarity: 50.0% Mismatches: 58
Query Match: 50.3% Indels: 3
DB: 2 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x US-09-177-234-2 (1-914)

QY 5 IleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePhe 24
DB 144 GTGCGTGACGAGCTGGCCATGGC---GGCAGCGGTGCCCAAGGCCATTTCTCATCTTT 200
QY 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
DB 201 GCTCGAGCACAAATGGAGCTGGATAACATGGGCTTATTGGTCGGGCCAGCTCTTCGAGGT 260
QY 45 GlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyProTy 62
DB 261 GGCTTAGAGGCGATCTTGGGTTCGAACACCTCTGGGTCAAGGGGTGGGCGCCATAT 320
QY 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82
DB 321 GCCGCCAACCTTAGGGCAATCTATTTCAGATGGAACACCTCTTAAGCCATCCAGGAG 380
QY 83 GlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 102
DB 381 ATGCTTAGCTGCTCCAAATTCGCGACACCAAGTCCCAAACTTAAGATTGTACAGGG 440
QY 103 GlyTySerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
DB 441 GGTATAGCCAAAGGTGTCACCTCGTGGCGCTGCTATTTCGCGATGTCAAGGCTTCAT 500
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyThrGlnAsnLeuGlnAsnArgGly 142
DB 501 CGACAAAGATTGTGGGAACCGTACTCTTTGGGTATCTTAAACAAACAGAGGAACGGA 560
QY 143 GlyIleAlaAsnTyProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
DB 561 CAGTAGAATACTACTCAACTGATCGGCTCGGGTTTACTGTAACTCGGAGACTTGATT 620
QY 163 CysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyThrIleGluAlaArgGly 182
DB 621 TGTGAAGGACCTTGATTGTTTACCACCACTCTTCTTATGGAGTCCAGGCTGCTGTT 680

```
QY 183 GLuAlaAlaArgPheLeuArgAspArgile 192
Db 681 CCAGTGTCCCGAGTCTCTCGCCACGAAGATC 710
RESULT 3
US-09-177-234-7
; Sequence 7, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; EARLIER FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (68)...(763)
; NAME/KEY: mat_peptide
; LOCATION: (161)...(763)
; NAME/KEY: sig_peptide
; LOCATION: (68)...(160)
US-09-177-234-7
Alignment Scores:
Pred. No.: 2.4e-48 Length: 999
Score: 499.50 Matches: 96
Percent Similarity: 67.4% Conservative: 32
Best Local Similarity: 50.5% Mismatches: 59
Query Match: 50.2% Indels: 3
DB: 3 Gaps: 2
US-08-817-997-2_COPY_36_229 (1-194) x US-09-177-234-7 (1-999)
QY 5 IleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuLeuPhe 24
Db 191 GTGCGTGAATGCAATGCGCAATGCG---GGCGGCGCGTGTCCCAAGGCCATCTCTCATCTTT 247
QY 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
Db 248 GCTAGAGGTACATGATGCGTGTATATGCTGGGCGCAGCTCTTGCAGGT 307
QY 45 GlyLeuGluSerHisIle-----ArgAsnIleTrrIleGlnGlyValGlyGlyProTyr 62
Db 308 GGCCTAGAGGTATGCTGGGTTCAATATACCTCTGGGTCCAGGTGTAGGTGGCCAATAT 367
QY 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82
Db 368 GCTGCCAATCTCGAGGCGCAATCTATTTCAGATGGGAACACCTCCCAAGGCCATCCAGGAG 427
QY 83 GlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 102
Db 428 ATGCTTAGTCTGCTCCAAATTAGGGGACCAAGTGTCCAAACCTCTAAGATTGTACAGGG 487
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaAlaValSerGluLeuSerGlyAlaVal 122
Db 183 GLuAlaAlaArgPheLeuArgAspArgile 192
Db 681 CCAGTGTCCCGAGTCTCTCGCCACGAAGATC 710
RESULT 4
US-09-177-234-5
; Sequence 5, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; EARLIER FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Verticillium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43)...(738)
; NAME/KEY: mat_peptide
; LOCATION: (133)...(738)
; NAME/KEY: sig_peptide
; LOCATION: (43)...(132)
US-09-177-234-5
Alignment Scores:
Pred. No.: 2.1e-46 Length: 869
Score: 482.00 Matches: 90
Percent Similarity: 68.0% Conservative: 33
Best Local Similarity: 49.7% Mismatches: 56
Query Match: 48.4% Indels: 2
DB: 3 Gaps: 1
US-08-817-997-2_COPY_36_229 (1-194) x US-09-177-234-5 (1-869)
QY 16 AlaCysProAspAlaLeuLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGly 35
Db 196 GCTTGGCCCCAAGGCTATCTCTCTCTTGTCTCGAGGACGATAGACTTGTATACATGGGC 255
QY 36 IleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIle 53
Db 256 TTATTGGTGGGCGCACCTCTTTCGACGCGTCTATCGGGGTATCTTGGGTTCACAAACCTC 315
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| | | | |
|-----|----|--|-----|
| 54 | QY | TpIleGInGlyValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArg | 73 |
| | | | |
| | | | |
| | | | |
| 316 | Db | TGGGTCAAAGCGTGGGTGGCCAATATGCTCAAGCTTGCAGGGTAATCTCTTTCCGGAT | 375 |
| | | | |
| | | | |
| | | | |
| 74 | QY | GlyThrSerGlnAlaAsnIleAspGluGlyIysArgLeuPheAlaLeuAlaAsnGlnIys | 93 |
| | | | |
| | | | |
| | | | |
| 376 | Db | GGGACCCCTCTCTCAAGCCATCCAGGAGATGATTACATTGCTCAATTGGCGGGATTA | 435 |
| | | | |
| | | | |
| | | | |
| 94 | QY | CysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAla | 113 |
| | | | |
| | | | |
| | | | |
| 436 | Db | TGTCCAAACTCCAGATTGTCACTGGGGGATATAGTCAAGTGCTGCTCTGTGGCGCA | 495 |
| | | | |
| | | | |
| | | | |
| 114 | QY | AlaValSerGluLeuSerGlyAlaValIysGluGlnValIysGlyValAlaLeuPheGly | 133 |
| | | | |
| | | | |
| | | | |
| 496 | Db | GCAATTCCGGATGTCAAGCTTCGATCCGACAGAAAGATTGTAGGAACGTGTA | 555 |
| | | | |
| | | | |
| | | | |
| 134 | QY | TyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLys | 153 |
| | | | |
| | | | |
| | | | |
| 556 | Db | TACTCCAAAAACAAACAGAGGAACGGTCAGGTAGAAAACTACTCTAATGACCGA | 615 |
| | | | |
| | | | |
| | | | |
| 154 | QY | ValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHis | 173 |
| | | | |
| | | | |
| | | | |
| 616 | Db | GTTTATTGCAACCTGGGGATTAAATTGCGAGGGGACCTTGATTGTTCTGCCACGTGCAC | 675 |
| | | | |
| | | | |
| | | | |
| 174 | QY | LeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArg | 193 |
| | | | |
| | | | |
| | | | |
| 676 | Db | CTCTCTTATGGAAACCAAGCTTCTGGTCTCTGCAGCAACAATTCCTCGCTAGTAAGATCAAT | 735 |
| | | | |
| | | | |
| | | | |
| 194 | QY | Ala 194 | |
| | | ::: | |
| 736 | Db | TCT 738 | |

```

RESULT 5
US-10-231-478-2
; Sequence 2, Application US/10231478
; Patent No. 6936445
; GENERAL INFORMATION:
; APPLICANT: KAWABE, TOMOYASU
; APPLICANT: KAMITAWARI, MASASHI
; TITLE OF INVENTION: ENZYME PREPARATION AND METHOD OF USING THE SAME
; FILE REFERENCE: 7372/73243
; CURRENT APPLICATION NUMBER: US/10/231,478
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: JP 2001-365495
; PRIOR FILING DATE: 2001-09-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(765)
US-10-231-478-2

```

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 9,286-21 |
| Score: | 260.00 |
| Percent Similarity: | 50.5% |
| Best Local Similarity: | 34.1% |
| Query Match: | 26.1% |
| DB: | 3 |
| Length: | 768 |
| Matches: | 62 |
| Conservative: | 30 |
| Mismatches: | 70 |
| Indels: | 20 |
| Gaps: | 6 |

US-08-817-997-2_COPY_36_229 (1-194) x US-10-231-478-2 (1-768)

| | | | |
|----|-----|--|-----|
| Qy | 11 | SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGlu | 30 |
| | : | : | : |
| | : | : | : |
| Db | 229 | ANGATTACTGGTGCCTGCACGATTACCGGTCTCTGCGCCGCGAACAGTGAG | 288 |
| | : | : | : |
| Qy | 31 | ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle | 50 |
| | : | : | : |
| | : | : | : |

| | | | |
|-----|--|---|-----|
| 289 | CCGGAACAGTTGGTGCTCTCGTCGGACCTCTCTGCTAGGCGCTTTGAGGAGCCGTC | 348 | |
| Qy | 51 | -----ArgAsnIleThrIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAlaThr | 68 |
| Db | 349 | GGTGGCTCCGCTTGAAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG | 402 |
| Qy | 69 | AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLyAsArgLeuPheAla | 88 |
| Db | 403 | GGATATTGGCTGGAGT-----GAAAGCCGCTGGCAGCAAGGCA | 441 |
| Qy | 89 | LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly | 102 |
| Db | 442 | ATGGCATCTCAGGCCAGCGACATCTCTCCAAGTGTCCGCACACCAAGCTTGTCATGACT | 501 |
| Qy | 103 | GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal | 122 |
| Db | 502 | GGCTATTCCAGGGCTCCAGATGTTTCACAAATGCCGTTGAGCACTCTCTCGCGAACAC | 561 |
| Qy | 123 | LysGluGlnValIysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly | 142 |
| Db | 562 | GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAAGGCGCAAG | 612 |
| Qy | 143 | GlyIleAlaAsnTyrProArgGluArgThrIysValPheCysAsnValGlyAspAlaVal | 162 |
| Db | 613 | GCTCTCCCAACAGTTGATGCTTCCCGGTCCACACTGTGTGTCACCGCTGCAGACACTATT | 672 |
| Qy | 163 | CysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly | 182 |
| Db | 673 | TGCAGAACAGCGTTATTATTCTCCCGCTCACTTGACTACGCTGTGTGATGTGCTTCT | 732 |
| Qy | 183 | GluAla | 184 |
| Db | 733 | CGCGCT | 738 |

RESULT 6
 US-09-585-468-2
 ; Sequence 2, Application US/09585468
 ; Patent No. 6537790
 ; GENERAL INFORMATION:
 ; APPLICANT: Sumitomo Chemical Co. Ltd.
 ; TITLE OF INVENTION: Esterase Genes and Use thereof
 ; FILE REFERENCE: P150409
 ; CURRENT APPLICATION NUMBER: US/09/585,468
 ; CURRENT FILING DATE: 2000-06-02
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO 2
 ; LENGTH: 798
 ; TYPE: DNA
 ; ORGANISM: Aspergillus flavus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) .. (768)
 US-09-585-468-2

| | | |
|------------------------|---------|---------------|
| Alignment Scores: | | |
| Pred. No.: | 9.8e-21 | Length: |
| Score: | 260.00 | Matches: |
| Percent Similarity: | 50.5% | Conservative: |
| Best Local Similarity: | 34.1% | Mismatches: |
| Query Match: | 26.1% | Indels: |
| DB: | 3 | Gaps: |
| | | 6 |
| | | 798 |

US-08-817-997-2 COPY 36 229 (1-194) x US-09-585-468-2 (1-798)

| | | | |
|----|-----|--|-----|
| Qy | 11 | SerGlyGerAlaAenAlaCysProAspAlaIleLeuIlePheAlaArgClySerThrGlu | 30 |
| Db | 229 | AATGGATTTACTGTGTGCTCGACGATTACACCGTTCTCTCCCGCGGAACCACTGAG | 288 |
| Qy | 31 | ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle | 50 |
| Db | 289 | CCCGGAACAGTTGTGTGTCTCGTCGACACTCTCTTGTGTAGCGCTTTGAGGAGCCGTC | 348 |
| Qy | 51 | -----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAlaThr | 68 |

```

Db      349  GGTGGCTCGCGCTTGGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402
Qy      69  AsnPhelLeuProArgGlyThrSerGlnAlaAsnIleAspGlyGlyLysArgLeuPheAla 88
Db      403  GGATATTGGCTGGAGGT-----GAAGCCGCTGGCAGCAAGGCA 441
Qy      89  LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db      442  ATGGCATCTCAGGCCAGGACATCTCTCCAGTGTCCGACACCAAGCTTGTATGAGT 501
Qy      103  GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db      502  GGCTATTCCAGGGCTGCCAGATTGTTCAATGCCGTTGAGCAACTTCTCTCGGACAC 561
Qy      123  LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db      562  GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAAGGGCAAG 612
Qy      143  GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db      613  GCTCTCCCAACGTTGATGCTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
Qy      163  CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db      673  TGGAGAACAGCGTTATTATTTGCGCGCTCACTTGACCTACCGTGTGTGATGGCTTCT 732

Qy      183  GluAla 184
Db      733  GCGGCT 738

```

RESULT 7

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US-10-114-115A-2
; Sequence 2, Application US/10114115A
; Patent No. 6812008
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: P150409
; CURRENT APPLICATION NUMBER: US/10/114,115A
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/585,468
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
US-10-114-115A-2

```

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Alignment Scores:
Pred. No.: 9.8e-21      Length: 798
Score: 260.00          Matches: 62
Percent Similarity: 50.5%      Conservative: 30
Best Local Similarity: 34.1%   Mismatches: 70
Query Match: 26.1%           Indels: 20
DB: 3                    Gaps: 6

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US-08-817-997-2_COPY_36_229 (1-194) x US-10-114-115A-2 (1-798)

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Qy      11  SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGlu 30
Db      229  AATGATTACTGGTGGCTGCCAGGATTACACCGTTCTCTTCCCGCGGAACCAAGT 288
Qy      31  ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
Db      289  CCGGAACGTTGGTGTCTCTGCGACCTCTCTTGTGAGCGGTTTGAGGAGCGGTC 348
Qy      51  -----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAlaThr 68
Db      349  GGTGGCTCGCGCTTGGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402

```

```

Db      349  GGTGGCTCGCGCTTGGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402
Qy      69  AsnPhelLeuProArgGlyThrSerGlnAlaAsnIleAspGlyGlyLysArgLeuPheAla 88
Db      403  GGATATTGGCTGGAGGT-----GAAGCCGCTGGCAGCAAGGCA 441
Qy      89  LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db      442  ATGGCATCTCAGGCCAGGACATCTCTCCAGTGTCCGACACCAAGCTTGTATGAGT 501
Qy      103  GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db      502  GGCTATTCCAGGGCTGCCAGATTGTTCAATGCCGTTGAGCAACTTCTCTCGGACAC 561
Qy      123  LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db      562  GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAAGGGCAAG 612
Qy      143  GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db      613  GCTCTCCCAACGTTGATGCTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
Qy      163  CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db      673  TGGAGAACAGCGTTATTATTTGCGCGCTCACTTGACCTACCGTGTGTGATGGCTTCT 732

Qy      183  GluAla 184
Db      733  GCGGCT 738

RESULT 8
US-10-114-116-2
; Sequence 2, Application US/10114116
; Patent No. 6828129
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: P150409
; CURRENT APPLICATION NUMBER: US/10/114,116
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US/09/585,468
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
US-10-114-116-2

Alignment Scores:
Pred. No.: 9.8e-21      Length: 798
Score: 260.00          Matches: 62
Percent Similarity: 50.5%      Conservative: 30
Best Local Similarity: 34.1%   Mismatches: 70
Query Match: 26.1%           Indels: 20
DB: 3                    Gaps: 6

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US-08-817-997-2_COPY_36_229 (1-194) x US-10-114-116-2 (1-798)

```

Qy      11  SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGlu 30
Db      229  AATGATTACTGGTGGCTGCCAGGATTACACCGTTCTCTTCCCGCGGAACCAAGT 288
Qy      31  ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
Db      289  CCGGAACGTTGGTGTCTCTGCGACCTCTCTTGTGAGCGGTTTGAGGAGCGGTC 348
Qy      51  -----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAlaThr 68
Db      349  GGTGGCTCGCGCTTGGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402

```


QY 48 SerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProTyrAspAlaLeuAla 67
|||
Db 193 TCGCAA-----GTTGGCGGGCGGTGCGATTGGGGTCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
|||
Db 229 GTGACTACCCAGCAGCAGCAGTACCGCGCGAGCGCGTCAACAGGTTCGATGATGCG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValAlaGlyGly 103
|||
Db 289 AGCGCCACATCCAGCGCAGCGTCCGCGAGTCCCGGACACACAGGATGTGCTGGTGGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuAlaValSerGluLeuSerGlyAlaValLys 123
|||
Db 349 TATTCCGAGGTCCGAGCGGTATGTTGTCACCTCGCGATGCCCGCGCGTGGCA 408
QY 124 GlnGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
|||
Db 409 GATCATGTCCCGCTGTGCGCCCTTTTCGGCGAGCCATCCAGTGTCTCCAGCATGTTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
|||
Db 469 TGGGCGCGGGTGGTTCGCGACATCGGTCCGCTGTATAGCTCTAAGACCATAACTTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
|||
Db 529 TGTGCTCCGACGATCAATATGACCGAGGCGGCAATATTATG---GGCATGTTTCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
|||
Db 586 TATGTTCAGTCCGGGATGACAGCCAGCGCGGACATTCGCGGACAGGCTC 639

RESULT 11

US-09-050-739-9
; Sequence 9, Application US/09050739
; Patent No. 6641814
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDRINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1054
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis

US-09-050-739-9

Alignment Scores:
Pred. No.: 2,14e-12 Length: 1054
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservative: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 3 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-09-050-739-9 (1-1054)
QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
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Db 276 GGCGGTGTGCGCGCATCGGATCCGTGTTCGGACATCGCGGTGCTTTTCGCTCGCGGC 335
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
|||
Db 336 AGCATCATCGGCTTCGCTTTGGC---GACGTCCGTGAGCGGTTCGCTACGACTCGCTACC 392
QY 48 SerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProTyrAspAlaLeuAla 67
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Db 393 TCGCAA-----GTTGGCGGGCGGTGCGATTCGGGTCTACGCG 428
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
|||
Db 429 GTGAACCTACCCAGCAGCAGCAGTACCGCGCGAGCGGTCAACCGTTCGCGATGATGCG 488
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValAlaGlyGly 103
|||
Db 489 AGCGCCACATCCAGCGCAGCGTCCGCGAGTTCACCTCGCGCATGCCCGCGGTGGCA 548
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
|||
Db 549 TATTCCGAGGTGCGAGCGGTCTCATGTTGTCACCTCGCGCATGCCCGCGGTGGCA 608
QY 124 GlnGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
|||
Db 609 GATCATGTCCGCGGTGTGCGCCCTTTTCGGCGAGCCATCCAGTGTGTTCTCCAGCATGTTG 668
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
|||
Db 669 TGGGCGCGGGTGGTTCGCGACATCGGTCCGCTGTATAGCTCTAAGACCATAACTTG 728
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
|||
Db 729 TGTGCTCCGACGATCCAATATGACCGGAGCGGCAATATTATG---GCGCATGTTTCG 785
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
|||
Db 786 TATGTTCAGTCCGGGATGACAGCCAGCGCGGACATTCGCGGCGGACAGGCTC 839

RESULT 12

US-08-390-878-17
; Sequence 17, Application US/08390878
; Patent No. 5700683
; GENERAL INFORMATION:
; APPLICANT: Stover, Charles K.
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,878
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 15371A-17

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-390-878-17

Alignment Scores:
Pred. No.: 9,24e-11 15239
Score: 189.50 61
Percent Similarity: 43.4% 25
Best Local Similarity: 30.8% 89
Query Match: 19.0% 23
DB: 2 7

US-08-817-997-2_COPY_36_229 (1-194) x US-08-390-878-17 (1-15239)

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QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 6702 AGCATCAGGCTCTGCTTGGC---GAGTCGGTGAGCGTTCGTCGACTGCTTACC 6758
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAla 67
DB 6759 TCGCAA-----GTTGGCGGCGGTGCGATTGGGGTCTACGCG 6794
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
DB 6795 GTGAACATACCCAGCAGCAGCACTACCGCGAGCGCGTCAAACGGTTCCGATGATCG 6854
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
DB 6855 AGGCCACATCAGCGGCGCGTCCGAGCTGCGCGAGCAGCAGGATGCTGCTGCTGCG 6914
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
DB 6915 TATTCGAGGTGCGAGCGTCATCGATTCTCCACCTCGCGCATCGCGCGGTTGCGCA 6974
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 6975 GATCATGTCGCGCTGTCGCCCTTTTCGCGAGCCATCCAGTGGTTTCTCCAGCATGTTG 7034
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 7035 TGGGCGGCGGTCGTGCGCAATCGGTCGCTGTATAGCTCTAGACCATATAACTTG 7094
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 7095 TGTGCTCCCGACGATCCATATGACCGAGGCGGCAATATTATG---GCGCATGTTTCG 7151
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
DB 7152 TATGTTTCAGTCGGGGATGACAGCCAGCGGCGGACATTCGCGCGAACAGGCTC 7205

RESULT 13

US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TUBERCULOSIS

FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 2,73e-07 4403765
Score: 189.50 61
Percent Similarity: 43.4% 25
Best Local Similarity: 30.8% 89
Query Match: 19.0% 23
DB: 3 7

US-08-817-997-2_COPY_36_229 (1-194) x US-09-103-840A-2 (1-4403765)

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QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 2225723 AGCATCAGGCTCTGCTTGGC---GAGTCGGTGAGCGTTCGTCGACTGCTTACC 2225667
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAla 67
DB 2225666 TCGCAA-----GTTGGCGGCGGTGCGATTGGGGTCTACGCG 2225631
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
DB 2225630 GTGAACATACCCAGCAGCAGCACTACCGCGAGCGCGTCAAACGGTTCCGATGATCG 2225571
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DB 2225570 AGGCCACATCAGCGGCGCGTCCGAGCTGCGCGAGCAGGATGCTGCTGCTGCG 2225511
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QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
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QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 2225390 TGGGCGGCGGTCGTGTCGCAATCGGTCGCTGTATAGCTCTAAGACCATATAACTTG 2225331
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 2225330 TGTGCTCCCGACGATCCATATGACCGAGGCGGCAATATTATG---GCGCATGTTTCG 2225274
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
DB 2225273 TATGTTTCAGTCGGGGATGACAGCCAGCGGCGGACATTCGCGCGAACAGGCTC 2225220

RESULT 14

US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.

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Qy 186 ArgPheLeuArgAspArgIleArg 193

Db |||::: ::::: 834 GACTTCGTTGCCGGAAGCTGCAA 857

Search completed: February 5, 2006, 00:07:16
Job time : 1567 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2006, 00:07:31 ; Search time 847 Seconds
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        1894.049 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229
Perfect score: 996
Sequence: 1 QLGAINGLESSANACPPA.....SYTIEARGEAAETLRDRA 194

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                  Listing first 45 summaries

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-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEADSIZE=500 -MTLEN=0 -MAXLEN=200000000 -HOST=abs06p
-USER=US08817997 @CGN_1_1549 @runat_03022006_161336_18217 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6 -FGAEXT=7
-YGAPOP=10 -YGAEXT=0.5 -DPOP=6 -DLEXT=7

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Database : Published Applications_NA_Main:*
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10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| | Score | Match | Length | | | |
| 1 | 519.5 | 52.2 | 2769 | 3 | US-09-923-760-5 | Sequence 5, Appl1 |
| 2 | 268.5 | 27.0 | 822 | 7 | US-10-424-599-33038 | Sequence 33038, Appl1 |
| 3 | 268.5 | 26.1 | 768 | 6 | US-10-331-478-2 | Sequence 2, Appl1 |
| 4 | 260 | 26.1 | 798 | 3 | US-09-999-170-1 | Sequence 1, Appl1 |
| 5 | 260 | 26.1 | 798 | 5 | US-10-114-116-2 | Sequence 2, Appl1 |
| 6 | 260 | 26.1 | 798 | 5 | US-10-114-115A-2 | Sequence 2, Appl1 |
| 7 | 274 | 21.1 | 874 | 8 | US-10-425-115-143033 | Sequence 143033, Appl1 |

| | | | | | | | |
|---|----|-------|------|------|---|----------------------|--------------------|
| C | 8 | 206 | 20.7 | 630 | 8 | US-10-425-115-62450 | Sequence 62450, A |
| | 9 | 189.5 | 19.0 | 651 | 3 | US-09-894-842-13 | Sequence 13, Appl |
| | 10 | 189.5 | 19.0 | 651 | 7 | US-10-388-902-13 | Sequence 13, Appl |
| | 11 | 189.5 | 19.0 | 651 | 7 | US-10-647-089-13 | Sequence 13, Appl |
| | 12 | 189.5 | 19.0 | 654 | 3 | US-09-855-604-258 | Sequence 258, Appl |
| | 13 | 189.5 | 19.0 | 654 | 3 | US-09-855-604-258 | Sequence 258, Appl |
| | 14 | 189.5 | 19.0 | 720 | 3 | US-09-855-604-260 | Sequence 260, Appl |
| | 15 | 189.5 | 19.0 | 720 | 3 | US-09-855-604-260 | Sequence 260, Appl |
| | 16 | 189.5 | 19.0 | 1054 | 3 | US-09-791-171-9 | Sequence 9, Appl |
| | 17 | 189.5 | 19.0 | 1054 | 3 | US-09-804-980-9 | Sequence 9, Appl |
| | 18 | 189.5 | 19.0 | 1054 | 6 | US-10-138-473-9 | Sequence 9, Appl |
| | 19 | 189.5 | 19.0 | 1054 | 7 | US-10-620-246-9 | Sequence 9, Appl |
| | 20 | 188.5 | 18.9 | 1060 | 3 | US-09-791-171-13 | Sequence 13, Appl |
| | 21 | 188.5 | 18.9 | 1060 | 3 | US-09-804-980-13 | Sequence 13, Appl |
| | 22 | 188.5 | 18.9 | 1060 | 7 | US-10-620-246-13 | Sequence 13, Appl |
| | 23 | 178 | 17.9 | 800 | 3 | US-09-791-171-51 | Sequence 51, Appl |
| | 24 | 178 | 17.9 | 800 | 3 | US-09-804-980-51 | Sequence 51, Appl |
| | 25 | 178 | 17.9 | 800 | 7 | US-10-620-246-51 | Sequence 51, Appl |
| | 26 | 167.5 | 16.8 | 950 | 3 | US-09-791-171-55 | Sequence 55, Appl |
| | 27 | 167.5 | 16.8 | 950 | 3 | US-09-804-980-55 | Sequence 55, Appl |
| | 28 | 167.5 | 16.8 | 950 | 6 | US-10-138-473-55 | Sequence 55, Appl |
| | 29 | 167.5 | 16.8 | 950 | 7 | US-10-620-246-55 | Sequence 55, Appl |
| | 30 | 130 | 13.1 | 1125 | 3 | US-09-880-505-153 | Sequence 153, App |
| | 31 | 130 | 13.1 | 1125 | 5 | US-10-051-643-153 | Sequence 153, App |
| | 32 | 130 | 13.1 | 1125 | 6 | US-10-025-979-8 | Sequence 8, Appl |
| | 33 | 124 | 12.4 | 856 | 8 | US-10-425-115-103843 | Sequence 103843, S |
| | 34 | 120.5 | 12.1 | 470 | 6 | US-10-259-678-157 | Sequence 157, App |
| | 35 | 120.5 | 12.1 | 795 | 8 | US-10-425-115-9562 | Sequence 9562, Ap |
| | 36 | 112 | 11.2 | 503 | 3 | US-09-880-505-111 | Sequence 111, App |
| | 37 | 112 | 11.2 | 503 | 5 | US-10-051-643-111 | Sequence 111, App |
| | 38 | 108 | 10.8 | 87 | 3 | US-09-873-075A-5 | Sequence 5, Appl |
| | 39 | 106 | 10.6 | 57 | 6 | US-10-232-544-86 | Sequence 86, Appl |
| | 40 | 106 | 10.6 | 665 | 8 | US-10-425-115-150352 | Sequence 150352, S |
| | 41 | 98 | 9.8 | 287 | 8 | US-10-653-047-1362 | Sequence 1362, Ap |
| C | 42 | 96 | 9.6 | 1555 | 5 | US-10-027-632-261569 | Sequence 261569, S |
| C | 43 | 96 | 9.6 | 1555 | 5 | US-10-027-632-261570 | Sequence 261570, S |
| C | 44 | 96 | 9.6 | 1555 | 6 | US-10-027-632-261569 | Sequence 261569, S |
| C | 45 | 96 | 9.6 | 1555 | 6 | US-10-027-632-261570 | Sequence 261570, S |

ALIGNMENTS

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RESULT 1
US-09-923-760-5
; Sequence 5, Application US/09923760
; Publication No. US20030119054A1
; GENERAL INFORMATION:
; APPLICANT: Mrksich, Milan
; APPLICANT: Hrneldand, Christian
; TITLE OF INVENTION: POLYPEPTIDE IMMOBILIZATION
; FILE REFERENCE: 7814/45
; CURRENT APPLICATION NUMBER: US/09/923,760
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2769
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-923-760-5

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| Pred. No.: | 7,89e-57 |
| Score: | 519.50 |
| Percent Similarity: | 65.4% |
| Best Local Similarity: | 50.0% |
| Query Match: | 52.2% |
| DB: | 3 |
| Length: | 2789 |
| Matches: | 107 |
| Conservative: | 33 |
| Mismatches: | 54 |
| Indels: | 20 |
| Gaps: | 3 |

US-08-817-997-2 COPY 36 229 (1-194) x US-09-923-760-5 (1-2769)

Qy 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19

Db 1051 CAGCTTGGTAGAACAACCTCGCAGCATGTGATCAACGGCAATAGCGCTTCCTGCGCCGAT 1110
Qy 20 AlarileuilePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- 36
Db 1111 GTCATCTTCAATTATGTCGCGAGGTTCAACAGAGACGGGCAACTTGGTTGCTAGAAATTCT 1170
Qy 37 -----ThrValGlyProAlaLeuAl 43
Db 1171 TCTCATGACAACATCATTCTTTCTTACATCATTCATTAGGAATCTCTGGTCTAGCAATTGC 1230
Qy 43 aAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyPr 61
Db 1231 CTCCAACTTGGAGTTCGCTCGCCCTCGGCAAGACGGTGTCTGATTCAGGGGTTGGCGGTGC 1290
Qy 61 oTyrAspAlaLaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAs 81
Db 1291 CTACGCAGCCACTCTTGGAGACAATGCTCTCCCTCGCGAACTCTTAGCGCGCAATCAG 1350
Qy 81 pGluGlyIysArgLeuPheAlaLeuAlaAsnGlnIysCysProAsnThrProValValAl 101
Db 1351 GGAGATGCTCGGTCTCTTCCAGCAGGCCCAACACCAAGTGCCCTGAGCGGACTTTGATCGC 1410
Qy 101 aGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAl 121
Db 1411 CGTGGCTACACCGAGGGTGTGCACTTCGACCGCCCTCCATCGAGGACTTCATCTCGGC 1470
Qy 121 aValIysGluGlnValIysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnAr 141
Db 1471 CATTCGTGACAAGATCGCGGAACTGTTCTGTTGGCTACACCAAGAACTACAGAACC 1530
Qy 141 gGlyGlyIleAlaAsnTyrProArgGluArgThrIysValPheCysAsnValGlyAspAl 161
Db 1531 TGGCCGAATCCCAACTACCTCGCGACAGGACCAAGGTCTTCTGCAATACAGGGGATCT 1590
Qy 161 aValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaAr 181
Db 1591 CGTTTGTATCTGTAGTCTGATCTGCTGCTGCACCTCACTTGGCTTATGGTCTGATGCTCG 1650
Qy 181 gGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 1651 TGGCCCTGCCCTGAGTTCCTCATCGAGAAGGTTGCGGCT 1690

RESULT 2

US-10-424-599-33038
; Sequence 33038, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285664
; SEQ ID NO 33038
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(822)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_129838C.1
US-10-424-599-33038

Alignment Scores:
Pred. No.: 1,08e-24 Length: 822
Score: 268.50 Matches: 74
Percent Similarity: 48.9% Conservative: 19

Best Local Similarity: 38.9% Mismatches: 76
Query Match: 27.0% Indels: 21
DB: 7 Gaps: 8
US-08-817-997-2_COPY_36_229 (1-194) x US-10-424-599-33038 (1-822)
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Db 244 GGAACACCTACACCAAGCTACCGACGGGACA-----CCTTCCGCGCCGTCACATG 297
Qy 23 IlePheAlaArgGlySerThrGluProGlyAsnMetGly-----IleThrValGlyPro 40
Db 298 GTGTATGCTCAGGAAGTCCAGGATGTTAACTGTGGAGACCCAGCTGCGTGGCGCG 357
Qy 41 AlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyVal 58
Db 358 ATCTTCTTCAACAACCTTGGCTCCGCACTGCTGCAACCTGGTGTCTCCAGGTTGT 417
Qy 59 GlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAla 78
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Db 454 GCGATCCCACTGGCAGCAGGACCATGCTGATCTGATCAACCGGCGCCGCAATGC 513
Qy 95 ProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAla 114
Db 514 CCAACACCAAGATTGTTCATCAGCGGCTACAGGCGAGGCGCCAGCTCGTCCACAACGCC 573
Qy 115 ValSerGluLeuSerGlyAlaValIysGluGlnValIysGlyValAlaLeuPheGlyTyr 134
Db 574 GCGGCGATGCTCTCTCTCCCTCGTGACCAACCGAGTCAACCGAGTGTACCTTCGGTGAC 633
Qy 135 ThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrIysVal 154
Db 634 CCGAGCGGAACCAAGCCCTTTTGGACCAATC-----CCTACAGCGCGACCCGCAATC 684
Qy 155 PheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeu 174
Db 685 TTCTGCGGTTTCAGGGGACAACTGATGATGGCGCATCATCATCCCCCGCGCACT 744
Qy 175 SerTyrThrIleGluAlaArgGlyGluAla 184
Db 745 CAGTACCAGCAAGACGCGCGCTGCTGCG 774
RESULT 3
US-10-231-478-2
; Sequence 2, Application US/10231478
; Publication No. US20030124683A1
; GENERAL INFORMATION:
; APPLICANT: KAWABE, TOMOYASU
; APPLICANT: KAMITAMARI, MASASHI
; TITLE OF INVENTION: ENZYME PREPARATION AND METHOD OF USING THE SAME
; FILE REFERENCE: 7372/73243
; CURRENT APPLICATION NUMBER: US/10/231,478
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: JP 2001-265495
; PRIOR FILING DATE: 2001-09-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(765)
US-10-231-478-2
Alignment Scores:
Pred. No.: 1.27e-23 Length: 768
Score: 260.00 Matches: 62

Percent Similarity: 50.5% Conservative: 30
Best Local Similarity: 34.1% Mismatches: 70
Query Match: 26.1% Indels: 20
DB: 6 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-231-478-2 (1-768)

QY 11 SerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGlySerThrGlu 30
DB 229 AATGATTTACTGGTCTGCACGGATTACACCGTTCTTCGCCCGCGAACCAGTGAG 288
QY 31 ProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeuGlySerHisIle 50
DB 289 CCGGAAACGTTGGTCTCGTCCGACCTCTTCCTGAGCGGTTGAGGAGCGGTC 348
QY 51 -----ArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAlaThr 68
DB 349 GGTGCGTCCGCTTGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402
QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
DB 403 GGATATTGGCTGGAGGT-----GAAAGCGCTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
DB 442 ATGGCATCTCAGCGCAGCGACATTCTCCAGGTCTCCGACCAAGCTTGTATGAGT 501
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
DB 502 GGTATTTCCAGGGCTGCCAGATTGTTCAATGCCGTTGAGCACTTCTTCGGGACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
DB 562 GCAAGCAAGATCAGCAGCGTCTCTTTTCGA-----GACCCATACAGGGCAAG 612
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
DB 613 GCTCTCCCAACGTTGATGCTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
DB 673 TGCAGAACAGCGTTATTATTCTGCCCGCTCACTTGACCTACGCTGTGTGAGTGGCTTCT 732

QY 183 GluAla 184
DB 733 GCGGCT 738

RESULT 4
US-09-999-170-1
; Sequence 1, Application US/09999170
; Publication No. US20030044894A1
; GENERAL INFORMATION:
; APPLICANT: KAWABE, TOMOYASU
; APPLICANT: KISHIMOTO HIRAMINE, KAE
; TITLE OF INVENTION: METHOD FOR STERILIZING TRANSFORMED CELLS
; FILE REFERENCE: 7372/72243
; CURRENT APPLICATION NUMBER: US/09/999,170
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: JP 2000-368180
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 798
; TYPE: DNA
; ORGANISM: ASPERGILLUS FLAVUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(768)
US-09-999-170-1

Alignment Scores: 1.34e-23 Length: 798
Pred. No.: 1.34e-23 Length: 798
Score: 260.00 Matches: 62

US-08-817-997-2_COPY_36_229 (1-194) x US-09-999-170-1 (1-798)

QY 11 SerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGlySerThrGlu 30
DB 229 AATGATTTACTGGTCTGCACGGATTACACCGTTCTTCGCCCGCGAACCAGTGAG 288
QY 31 ProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeuGlySerHisIle 50
DB 289 CCGGAAACGTTGGTCTCGTCCGACCTCTTCCTGAGCGGTTGAGGAGCGGTC 348
QY 51 -----ArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAlaThr 68
DB 349 GGTGCGTCCGCTTGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402
QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
DB 403 GGATATTGGCTGGAGGT-----GAAAGCGCTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
DB 442 ATGGCATCTCAGCGCAGCGACATTCTTCAGAGTCTCCGACCAAGCTTGTATGAGT 501
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
DB 502 GGTATTTCCAGGGCTGCCAGATTGTTCAATGCCGTTGAGCACTTCTTCGGGACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
DB 562 GCAAGCAAGATCAGCAGCGTCTCTTTTCGA-----GACCCATACAGGGCAAG 612
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
DB 613 GCTCTCCCAACGTTGATGCTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
DB 673 TGCAGAACAGCGTTATTATTCTGCCCGCTCACTTGACCTACGCTGTGTGAGTGGCTTCT 732

QY 183 GluAla 184
DB 733 GCGGCT 738

RESULT 5
US-10-114-116-2
; Sequence 2, Application US/10114116
; Publication No. US20020164727A1
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: P150409
; CURRENT APPLICATION NUMBER: US/10/114,116
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US/09/585,468
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
US-10-114-116-2

Alignment Scores: 1.34e-23 Length: 798
Pred. No.: 1.34e-23 Length: 798
Score: 260.00 Matches: 62

Percent Similarity: 50.5%
 Best Local Similarity: 34.1%
 Query Match: 26.1%
 DB: 5

US-08-817-997-2_COPY_36_229 (1-194) x US-10-114-116-2 (1-798)

Qy 11 SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaAArgGlySerThrGlu 30
 Db 229 AATGGATTTACTGGTCCCTGCAGGATTACACCGTTCTCTTCGCCCGGGAACAGTGG 288
 Qy 31 ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
 Db 289 CCGGAAACGTTGGTGTCTCTCGTCCGACCTCTCTTGTGAGCGCTTTGAGGGAGCCGTC 348
 Qy 51 -----ArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAlaThr 68
 Db 349 GGTGCTCCGCTTGAGCTTCAGGCTTCAACGGC---TATTCTGCATCTGTC---GAG 402
 Qy 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
 Db 403 GGATATTGGCTGGAGGT-----GAAGCCGCTGGCAGCAAGGCA 441
 Qy 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
 Db 442 ATGGCATCTCAGGCCAGCAGACATTCTCTCCAGTGTCCCGACCAAGCTTGTCTAGT 501
 Qy 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
 Db 502 GGTATTCCAGGGCTCCAGATTGTTTCAATGCGCTTGACCACTTCTCGGGAACAC 561
 Qy 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
 Db 562 GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAAGGGCAAG 612
 Qy 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
 Db 613 GCTCTCCCAACGTTGATGTTCCCGCTCCCACTGTGTGCGCAGTGGAGACACTATT 672
 Qy 163 CysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
 Db 673 TGGAGAACAGCGTTATTATTCTGCCCGCTCACTTGACCTACGCTGTGATGGCTTCT 732
 Qy 183 GluAla 184
 Db 733 GCGGCT 738

RESULT 6
 US-10-114-115A-2
 ; Sequence 2, Application US/10114115A
 ; Publication No. US20020173013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sumitomo Chemical Co. Ltd.
 ; TITLE OF INVENTION: Esterase Genes and Use thereof
 ; FILE REFERENCE: P150409
 ; CURRENT APPLICATION NUMBER: US/10/114,115A
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO 2
 ; LENGTH: 798
 ; TYPE: DNA
 ; ORGANISM: Aspergillus flavus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(768)
 US-10-114-115A-2

Alignment Scores: 1.34e-23 Length: 798
 Pred. No.: 260.00 Matches: 62
 Score: 50.5% Conservative: 30
 Percent Similarity: 50.5%


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; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-13

Alignment Scores:
Pred. No.: 1-72e-14 Length: 651
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservatives: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-09-894-844-13 (1-651)
QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
DB 76 GCGCGTGTGCGCGCATCGATCGGTGTTCGACATCGCGTGTTCGCTCGCGGC 135
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaLeuGlu 47
DB 136 ACGCATCAGGCTTCTGCTTGGC---GACGTGCGTGAGCGTTCGTCGACTCGCTTACC 192
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAla 67
DB 193 TCGCAA-----GTTGGCGGCGGTGCGATTCGGGTCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
DB 229 GTGAACCTACCCAGCAGCAGCTACCGCGCGAGCGGTCAAAAGGTTCCGATGATCG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 103
DB 289 AGCGCCACATCCAGCGCACCGTCCGACGTGCCAGCTGCCGACACACAGGATTCGTGGTGGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
DB 349 TATTCGAGGTGCGAGCGGTATTCGATTCACCTCGCGATGCCGCGCGCGGTGGCA 408
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 409 GATCATGTCCGCGCTGTGCGCTTTTCGCGGAGCCATCCAGTGGTTCTCCAGCATGTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 469 TGGGCGCGGCGGTGTTCGCAATTCGTCGCGAGCCATCCAGTGGTTCTCCAGCATGTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 529 TGTGCTCCGACGATCCAATATGACCGAGCGGCGCAATATTATG---GCGCATGTTCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
DB 586 TATGTTTCAGTCGCGGATGACAGCCAGCGCGGCGACATTCGCGCGGACAGGCTC 639

RESULT 11
US-10-647-089-13
; Sequence 13, Application US/10647089
; Publication No. US20040063923A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
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; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-647-089-13

Alignment Scores:
Pred. No.: 1.72e-14 Length: 651
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservative: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-647-089-13 (1-651)
QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
DB 76 GCGGTCGTGCGCGCATCGGATCCGTCGTTCGGACATCCGCGTCGTTTCGCTCGCGGC 135
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 136 AGCATCAGGCTCTCGTCTTGGC---GAGTCGCTGAGCGGTCGTCGACTCGCTTACC 192
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAla 67
DB 193 TCGCAA-----GTTGGCGGGCGGTCGATTGGGGCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGly 83
DB 229 GTGAACCTACCAGCAAGCAGCAGCTACCGCGGAGCGGTCGTCGATGATGCG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 103
DB 289 AGCGCCACATCCAGCGCAGCGTCGCCAGCTGCCGACACACCGAGATTGTGCTTGGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVallys 123
DB 349 TATTCGAGGTGGCAGCTCATCGATTGTTCACCTCGCGATGCCGCGCGGTGGCA 408
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 409 GATCATGTCGCGCTGCGCCCTTTTCGGCGAGCCATCCAGTGGTTTCTCCAGCATGTTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 469 TGGGCGCGGGTGGTTCGCGCAATCGTCGCTGTATAGCTCTAAGACCAATAACTTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 529 TGTGCTCCGAGCATCAATATGACCGGAGCGGCGCAATATTATG---GGCATGTTTCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
DB 586 TATGTTCACTCGGGATGACAAGCCAGCGCGGACATTCGCGCGCAACAGGCTC 639

RESULT 12
US-09-855-604-258
; Sequence 258, Application US/09855604
; Publication No. US20040214165A1
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: FORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES

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; APPLICANT: GOGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(651)
US-09-855-604-258

Alignment Scores:
Pred. No.: 1.73e-14 Length: 654
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservative: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-09-855-604-258 (1-654)
QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
DB 76 GCGGTCGTGCGCGCATCGGATCCGTCGTTCGGACATCCGCGTCGTTTCGCTCGCGGC 135
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 136 AGCATCAGGCTCTCGTCTTGGC---GAGTCGCTGAGCGGTCGTCGACTCGCTTACC 192
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAla 67
DB 193 TCGCAA-----GTTGGCGGGCGGTCGATTGGGGCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGly 83
DB 229 GTGAACCTACCAGCAAGCAGCAGCTACCGCGGAGCGGTCGTCGATGATGCG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 103
DB 289 AGCGCCACATCCAGCGCAGCGTCGCCAGCTGCCGACACACCGAGATTGTGCTTGGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVallys 123
DB 349 TATTCGAGGTGGCAGCTCATCGATTGTTCACCTCGCGATGCCGCGCGGTGGCA 408
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 409 GATCATGTCGCGCTGCGCCCTTTTCGGCGAGCCATCCAGTGGTTTCTCCAGCATGTTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 469 TGGGCGCGGGTGGTTCGCGCAATCGTCGCTGTATAGCTCTAAGACCAATAACTTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 529 TGTGCTCCGAGCATCAATATGACCGGAGCGGCGCAATATTATG---GGCATGTTTCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192

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Qy 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
Db 295 GTGAACACTACCCAGCAAGACGACTACCGCGCGCGCGTCAACCGTTCCTCCGATGATGCG 354
Qy 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
Db 355 AGCGCCACATCCAGCGCACCGTCGCGAGTGCCTCCGACACACCGAGGATTGTGCTGTGTCGC 414
Qy 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 415 TATTCGCGGGTGCAGCGGTCTGATGTTTCCACCTCGCGCATCGCGCCGCGGTGGCA 474
Qy 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
Db 475 GATCATGTGCGCGCTGCTCGCCCTTTTCGCGAGCCATCCAGTGTGTTCTCCAGCATGTTG 534
Qy 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
Db 535 TGGGGCGCGGGTCTGTTGCGCAATCGGTCCGCTGTATAGCTCTAAGACCATAAACTTG 594
Qy 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
Db 595 TGTGCTCCGAGATCCATATATGACCGGAGCGGCGCAATATTATG---GGCATGTTTCG 651
Qy 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
Db 652 TATGTTTCAGTCGGGGATGATCAAGCCAGCGCGGACATTCGCGCGCAAGGCTC 705

RESULT 15
US-09-855-604-260
; Sequence 260, Application US/09855604
; Publication No. US20050158714A9
; GENERAL INFORMATION:
; APPLICANT: GICOUEL, BRIGITTE
; APPLICANT: FORTNOL, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: GOGUET DE LA SALMONIERRE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; FILE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 260
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(717)
US-09-855-604-260

Alignment Scores:
Pred. No.: 1.98e-14 Length: 720
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservative: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 3 Gaps: 7
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US-08-817-997-2_COPY_36_229 (1-194) x US-09-855-604-260 (1-720)
Qy 8 GlyLeuGluSerGlySerAlaAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
Db 142 GCGGTCGTCGCGCGCATCGGATCCGCTGTTCCGACATCGCGGTCTTTTCCTCGCGGC 201
Qy 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
Db 202 AGCATCAGGCTTCGTCTTGGC---GACGTGCTGAGCGCTTCGTGCTGACTCGCTTACC 258
Qy 48 SerHisIleArgAsnIleTyrIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAla 67
Db 259 TCGCAA-----CTTGGCGGCGGTCTGATGGGTCTACGCG 294
Qy 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
Db 295 GTGAACACTACCCAGCAAGACGACTACCGCGCGCGCGTCAACCGTTCCTCCGATGATGCG 354
Qy 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
Db 355 AGCGCCACATCCAGCGCACCGTCGCGAGTGCCTCCGACACACCGAGGATTGTGCTGTGTCGC 414
Qy 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 415 TATTCGCGGGTGCAGCGGTCTGATGTTTCCACCTCGCGCATCGCGCCGCGGTGGCA 474
Qy 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
Db 475 GATCATGTGCGCGCTGCTCGCCCTTTTCGCGAGCCATCCAGTGTGTTCTCCAGCATGTTG 534
Qy 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
Db 535 TGGGGCGCGGGTCTGTTGCGCAATCGGTCCGCTGTATAGCTCTAAGACCATAAACTTG 594
Qy 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
Db 595 TGTGCTCCGAGATCCATATATGACCGGAGCGGCGCAATATTATG---GGCATGTTTCG 651
Qy 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
Db 652 TATGTTTCAGTCGGGGATGATCAAGCCAGCGCGGACATTCGCGCGCAAGGCTC 705
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Search completed: February 5, 2006, 01:57:36

Job time : 851 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2006, 00:19:19 ; Search time 239 Seconds
(without alignments)
680.277 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPD.....SYTIARGEAEARFLDEIRA 194

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6068529 seqs, 41903697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications_NA_New -QFMT=fastcap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abes04
-USER=US08817997_@CGN_1_1_220_@runat_03022006_161338_18239 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA_New:

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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
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10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 189.5 | 19.0 | 651 | 8 | US-11-143-401-13 |
| 2 | 189.5 | 19.0 | 654 | 8 | US-11-052-554A-710 |
| 3 | 120.5 | 12.1 | 470 | 7 | US-10-802-796-157 |
| 4 | 91 | 9.1 | 420 | 7 | US-10-802-796-496 |
| 5 | 89 | 8.9 | 5706 | 8 | US-11-052-554A-519 |
| 6 | 87 | 8.7 | 1253 | 6 | US-10-838-616-17 |
| | | | | | Sequence 13, Appl |
| | | | | | Sequence 710, App |
| | | | | | Sequence 157, App |
| | | | | | Sequence 496, App |
| | | | | | Sequence 519, App |
| | | | | | Sequence 17, Appl |

| | | | | | | | |
|---|----|------|-----|--------|----|---------------------|-------------------|
| c | 7 | 84.5 | 8.5 | 37507 | 7 | US-10-522-037-2 | Sequence 2, Appli |
| c | 8 | 82.5 | 8.3 | 414 | 7 | US-10-467-657-2927 | Sequence 2927, Ap |
| c | 9 | 82 | 8.2 | 1093 | 7 | US-10-750-185-27797 | Sequence 27797, A |
| c | 10 | 82 | 8.2 | 1093 | 7 | US-10-750-185-27797 | Sequence 27797, A |
| c | 11 | 81 | 8.1 | 96988 | 8 | US-11-117-187-196 | Sequence 196, App |
| c | 12 | 80.5 | 8.1 | 169047 | 8 | US-11-121-086-15 | Sequence 15, Appl |
| c | 13 | 80 | 8.0 | 1188 | 6 | US-10-838-616-25 | Sequence 25, Appl |
| c | 14 | 79.5 | 8.0 | 4146 | 8 | US-11-052-554A-522 | Sequence 522, App |
| c | 15 | 79 | 7.9 | 445 | 7 | US-10-802-796-75 | Sequence 75, Appl |
| c | 16 | 79 | 7.9 | 1893 | 7 | US-10-517-939-41 | Sequence 41, Appl |
| c | 17 | 79 | 7.9 | 2196 | 8 | US-11-052-554A-539 | Sequence 539, App |
| c | 18 | 78.5 | 7.9 | 2406 | 8 | US-11-052-554A-550 | Sequence 550, App |
| c | 19 | 78.5 | 7.9 | 3990 | 8 | US-11-052-554A-520 | Sequence 520, App |
| c | 20 | 78.5 | 7.9 | 79528 | 7 | US-10-276-233A-6 | Sequence 6, Appli |
| c | 21 | 78 | 7.8 | 153376 | 8 | US-11-121-086-5 | Sequence 5, Appli |
| c | 22 | 78 | 7.8 | 172543 | 8 | US-11-121-086-6 | Sequence 6, Appli |
| c | 23 | 77.5 | 7.8 | 351 | 7 | US-10-467-657-2929 | Sequence 2929, Ap |
| c | 24 | 77 | 7.7 | 879 | 8 | US-11-136-527-2695 | Sequence 2695, Ap |
| c | 25 | 77 | 7.7 | 950 | 7 | US-10-750-185-53331 | Sequence 53331, A |
| c | 26 | 77 | 7.7 | 950 | 7 | US-10-750-185-53331 | Sequence 53331, A |
| c | 27 | 77 | 7.7 | 1725 | 8 | US-11-185-342-2 | Sequence 2, Appli |
| c | 28 | 77 | 7.7 | 2210 | 7 | US-11-185-342-1 | Sequence 1, Appli |
| c | 29 | 77 | 7.7 | 3301 | 7 | US-10-750-185-42771 | Sequence 42771, A |
| c | 30 | 77 | 7.7 | 3301 | 7 | US-10-750-185-42771 | Sequence 42771, A |
| c | 31 | 76.5 | 7.7 | 1308 | 7 | US-10-467-657-7577 | Sequence 7577, Ap |
| c | 32 | 76.5 | 7.7 | 2837 | 7 | US-10-750-185-54633 | Sequence 54633, A |
| c | 33 | 76.5 | 7.7 | 2837 | 7 | US-10-750-185-54633 | Sequence 54633, A |
| c | 34 | 76.5 | 7.7 | 116856 | 8 | US-11-143-980-1 | Sequence 1, Appli |
| c | 35 | 76 | 7.6 | 333 | 7 | US-10-802-796-723 | Sequence 723, App |
| c | 36 | 76 | 7.6 | 2133 | 8 | US-11-143-980-13 | Sequence 13, Appl |
| c | 37 | 76 | 7.6 | 5242 | 7 | US-10-750-185-24846 | Sequence 24846, A |
| c | 38 | 76 | 7.6 | 5242 | 7 | US-10-750-185-24846 | Sequence 24846, A |
| c | 39 | 76 | 7.6 | 116856 | 8 | US-11-143-980-1 | Sequence 1, Appli |
| c | 40 | 75.5 | 7.6 | 525 | 8 | US-11-059-222-7 | Sequence 7, Appli |
| c | 41 | 75.5 | 7.6 | 525 | 10 | US-11-058-976-7 | Sequence 7, Appli |
| c | 42 | 75.5 | 7.6 | 3873 | 7 | US-10-750-185-30606 | Sequence 30606, A |
| c | 43 | 75.5 | 7.6 | 3873 | 7 | US-10-750-185-30606 | Sequence 30606, A |
| c | 44 | 75.5 | 7.6 | 4983 | 8 | US-11-052-554A-521 | Sequence 521, App |
| c | 45 | 75.5 | 7.6 | 6014 | 8 | US-11-102-476-45 | Sequence 45, Appl |

ALIGNMENTS

RESULT 1

US-11-143-401-13
; Sequence 13, Application US/11143401
; Publication No. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-13

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: February 5, 2006, 00:19:19 ; Search time 239 Seconds
(without alignments)
680.277 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPD.....SYTIEARGEARFLRDIRA 194

Scoring table:

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| Ygapop 10.0 , Ygapext 0.5 | |
| Fgapop 6.0 , Fgapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
5: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/prodata/2/pubpna/US12_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 189.5 | 19.0 | 651 | 8 US-11-143-401-13 | Sequence 13, Appl |
| 2 | 189.5 | 19.0 | 654 | 8 US-11-052-554A-710 | Sequence 710, App |
| 3 | 120.5 | 12.1 | 470 | 7 US-10-802-796-157 | Sequence 157, App |
| 4 | 91 | 9.1 | 420 | 7 US-10-802-796-496 | Sequence 496, App |
| 5 | 89 | 8.9 | 5706 | 8 US-11-052-554A-519 | Sequence 519, App |
| 6 | 87 | 8.7 | 1253 | 6 US-10-838-616-17 | Sequence 17, Appl |

| | | | | | |
|------|-----|--------|----|---------------------|-------------------|
| 84.5 | 8.5 | 37507 | 7 | US-10-522-037-2 | Sequence 2, Appli |
| 82.5 | 8.3 | 414 | 7 | US-10-467-657-2927 | Sequence 2927, Ap |
| 82 | 8.2 | 1093 | 7 | US-10-750-185-27797 | Sequence 27797, A |
| 82 | 8.2 | 1093 | 7 | US-10-750-623-27797 | Sequence 27797, A |
| 81 | 8.1 | 96988 | 8 | US-11-117-187-196 | Sequence 196, App |
| 80.5 | 8.1 | 169047 | 8 | US-11-121-086-15 | Sequence 15, Appl |
| 80 | 8.0 | 1188 | 6 | US-10-838-616-25 | Sequence 25, Appl |
| 79.5 | 8.0 | 4145 | 8 | US-11-052-554A-522 | Sequence 522, App |
| 79 | 7.9 | 445 | 7 | US-10-802-796-75 | Sequence 75, Appl |
| 79 | 7.9 | 1893 | 7 | US-10-517-939-41 | Sequence 41, Appl |
| 79 | 7.9 | 2196 | 8 | US-11-052-554A-539 | Sequence 539, App |
| 78.5 | 7.9 | 2406 | 8 | US-11-052-554A-550 | Sequence 550, App |
| 78.5 | 7.9 | 3990 | 8 | US-11-052-554A-520 | Sequence 520, App |
| 78.5 | 7.9 | 79528 | 7 | US-10-276-233A-6 | Sequence 6, Appli |
| 78 | 7.8 | 153376 | 8 | US-11-121-086-5 | Sequence 5, Appli |
| 78 | 7.8 | 172543 | 8 | US-11-121-086-6 | Sequence 6, Appli |
| 77.5 | 7.8 | 351 | 7 | US-10-467-657-2929 | Sequence 2929, Ap |
| 77 | 7.7 | 879 | 8 | US-11-136-527-2695 | Sequence 2695, Ap |
| 77 | 7.7 | 950 | 7 | US-10-750-185-5331 | Sequence 5331, A |
| 77 | 7.7 | 950 | 7 | US-10-750-623-5331 | Sequence 5331, A |
| 77 | 7.7 | 1725 | 8 | US-11-185-342-2 | Sequence 2, Appli |
| 77 | 7.7 | 2210 | 8 | US-11-185-342-1 | Sequence 1, Appli |
| 77 | 7.7 | 3301 | 7 | US-10-750-185-42771 | Sequence 42771, A |
| 77 | 7.7 | 3301 | 7 | US-10-750-623-42771 | Sequence 42771, A |
| 76.5 | 7.7 | 1308 | 7 | US-10-467-657-7577 | Sequence 7577, Ap |
| 76.5 | 7.7 | 2837 | 7 | US-10-750-185-54633 | Sequence 54633, A |
| 76.5 | 7.7 | 2837 | 7 | US-10-750-623-54633 | Sequence 54633, A |
| 76.5 | 7.7 | 116856 | 8 | US-11-143-980-1 | Sequence 1, Appli |
| 76 | 7.6 | 333 | 7 | US-10-802-796-723 | Sequence 723, App |
| 76 | 7.6 | 2133 | 8 | US-11-143-980-13 | Sequence 13, Appl |
| 76 | 7.6 | 5242 | 7 | US-10-750-185-24846 | Sequence 24846, A |
| 76 | 7.6 | 5242 | 7 | US-10-750-623-24846 | Sequence 24846, A |
| 76 | 7.6 | 116856 | 8 | US-11-143-980-1 | Sequence 1, Appli |
| 75.5 | 7.6 | 525 | 8 | US-11-059-222-7 | Sequence 7, Appli |
| 75.5 | 7.6 | 525 | 10 | US-11-058-976-7 | Sequence 7, Appli |
| 75.5 | 7.6 | 3873 | 7 | US-10-750-185-30606 | Sequence 30606, A |
| 75.5 | 7.6 | 3873 | 7 | US-10-750-623-30606 | Sequence 30606, A |
| 75.5 | 7.6 | 4983 | 8 | US-11-052-554A-521 | Sequence 521, App |
| 75.5 | 7.6 | 6014 | 8 | US-11-102-476-45 | Sequence 45, Appl |

ALIGNMENTS

RESULT 1

US-11-143-401-13
; Sequence 13, Application US/11143401
; Publication No. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary A.
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-13

Alignment Scores: 1.3e-11 Length: 651
 Pred. No.: 189.50 Matches: 61
 Score: 189.50
 Percent Similarity: 43.4% Conservative: 25
 Best Local Similarity: 30.8% Mismatches: 89
 Query Match: 19.0% Indels: 23
 DB: 8 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-11-143-401-13 (1-651)

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 QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
 DB 136 ACCGATCAGGCTCTGGTCTTGGC---GAGTCGGTGAGCGGTTCGCACTCGCTTACC 192
 QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAla 67
 DB 193 TCGCAA-----GTTGGCGGCGGTTCGATTGGGGTCTACGCG 228
 QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
 DB 229 GTGAATACCCAGCAAGCGACGACTACCGCGCGAGCGGTCAAACGGTTCGATGATGCG 288
 QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
 DB 289 AGCGCCACATCCAGCGCACCGTCGCCAGCTGCCCCGACACACAGGATTGTGCTTGGTGC 348
 QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaValSerGluLeuSerGlyAlaValLys 123
 DB 349 TATTCGAGGTGCGAGCGGTCTCGATTGTTCACCTCGCGCATCGCGCGGTGGCA 408
 QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
 DB 409 GATCATGTGCGCGCTGCGCCCTTTTCGGCGAGCCATCCAGTGGTTCCTCCAGCATGTTG 468
 QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
 DB 469 TGGGGCGGGGTGCTTGGCAATCGTCCGCTGTATAGCTCTAAGACCATAACTTG 528
 QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
 DB 529 TGTGCTCCGACGATCCATATGACCGGAGCGGCAATATTATG---GCGCATGTTTCG 585
 QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
 DB 586 TATGTTTCAGTCGGGGATGACAGCCAGCGCGGACATTCGCGCGAAGGCTC 639

RESULT 2
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 ; Sequence 710, Application US/11052554A
 ; Publication No. US2005028866A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sachdeva, et al.
 ; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
 ; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
 ; FILE REFERENCE: 30853/40359A
 ; CURRENT APPLICATION NUMBER: US/11/052,554A
 ; CURRENT FILING DATE: 2005-02-07
 ; PRIOR APPLICATION NUMBER: US 60/589,227
 ; PRIOR FILING DATE: 2004-07-20
 ; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
 ; PRIOR FILING DATE: 2004-02-06
 ; NUMBER OF SEQ ID NOS: 763
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 710
 ; LENGTH: 654
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis H37Rv
 ; US-11-052-554A-710

Alignment Scores: 1.31e-11 Length: 654
 Pred. No.: 189.50 Matches: 61
 Score: 189.50
 Percent Similarity: 43.4% Conservative: 25
 Best Local Similarity: 30.8% Mismatches: 89
 Query Match: 19.0% Indels: 23
 DB: 8 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-11-052-554A-710 (1-654)

QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
 DB 76 GGCGGTCTGCGCGCATCGGATCGGTTCGACATCGCGTCTTTCGCTCGCGGC 135
 QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
 DB 136 ACCGATCAGGCTCTGGTCTTGGC---GAGTCGGTGAGCGGTTCGCACTCGCTTACC 192
 QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAla 67
 DB 193 TCGCAA-----GTTGGCGGCGGTTCGATTGGGGTCTACGCG 228
 QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
 DB 229 GTGAATACCCAGCAAGCGACGACTACCGCGCGAGCGGTCAAACGGTTCGATGATGCG 288
 QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
 DB 289 AGCGCCACATCCAGCGCACCGTCGCCAGCTGCCCCGACACACAGGATTGTGCTTGGTGC 348
 QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaValSerGluLeuSerGlyAlaValLys 123
 DB 349 TATTCGAGGTGCGAGCGGTCTCGATTGTTCACCTCGCGCATCGCGCGGTGGCA 408
 QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
 DB 409 GATCATGTGCGCGCTGCGCCCTTTTCGGCGAGCCATCCAGTGGTTCCTCCAGCATGTTG 468
 QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
 DB 469 TGGGGCGGGGTGCTTGGCAATCGTCCGCTGTATAGCTCTAAGACCATAACTTG 528
 QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
 DB 529 TGTGCTCCGACGATCCATATGACCGGAGCGGCAATATTATG---GCGCATGTTTCG 585
 QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
 DB 586 TATGTTTCAGTCGGGGATGACAGCCAGCGCGGACATTCGCGCGAAGGCTC 639

RESULT 3
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 ; Sequence 157, Application US/10802796
 ; Publication No. US20050250104A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COLE, STEWART
 ; APPLICANT: BUCHRIESEN-BROSCH, ROLAND
 ; APPLICANT: GORDON, STEPHEN
 ; APPLICANT: BILLAULT, ALAIN
 ; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
 ; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
 ; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
 ; FILE REFERENCE: 05394.0011-00000
 ; CURRENT APPLICATION NUMBER: US/10/802,796
 ; CURRENT FILING DATE: 2004-03-18
 ; PRIOR APPLICATION NUMBER: US/09/673,476
 ; PRIOR FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: PCT/IB99/00740
 ; PRIOR FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: 09/060,756
 ; PRIOR FILING DATE: 1998-04-16
 ; NUMBER OF SEQ ID NOS: 743

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; SEQ ID NO 157
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (331)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (362)
; OTHER INFORMATION: a, t, c or g
US-10-802-796-157

Alignment Scores:
Pred. No.: 0.000518 Length: 470
Score: 120.50 Matches: 41
Percent Similarity: 46.1% Conservative: 12
Best Local Similarity: 35.7% Mismatches: 41
Query Match: 12.1% Indels: 21
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-802-796-157 (1-470)
QY 94 CysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAla-----Leu 110
Db 114 TGC CGG GGC CAC GAG GTT GCT CCG CGG TACT CCG CAG GGT GCG CGT GAT CGA CAT C 173
QY 111 IleAlaAlaAla-----ValSerGluLeuSerGlyAlaValLys 123
Db 174 GTC ACC GCG CAC CAC TAC TCG CGG CCG TGT TCG CAG CCG GTT GCG CGC GCG GAG C 233
QY 124 GluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGly 143
Db 234 GAT CAT CAC TCG CGG GAT CGC CTT GTT TCG G-----AAT CCT CGG CGC GCG TGG C 284
QY 144 -----IleAlaAsnTyrProArg-----GluArgThrLysValPheCysAsnVal 158
Db 285 GGC TGT GAT GAG CGC CCG TCA TCG GGT TCC AAG ACC CAT CAC CTT CTG CAACAAC 344
QY 159 GlyAspAlaValCysThr---GlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db 345 GGC GAC CCG CAG ATT GTT CNG ACG CCA CCG-----TGG CAG CGC CAC CTAGG CTAG TG 398
QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
Db 399 CCG CGG GAT GAC CAAC CAG CGC GCG GTT TCG TCG CAG CAG GAT C 443

RESULT 4
US-10-802-796-496
; Sequence 496, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHNER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2

; SEQ ID NO 496
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (21)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (23)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (106)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (200)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (272)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (355)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (362)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (413)
; OTHER INFORMATION: a, t, c or g
US-10-802-796-496

Alignment Scores:
Pred. No.: 0.952 Length: 420
Score: 91.00 Matches: 29
Percent Similarity: 43.0% Conservative: 8
Best Local Similarity: 33.7% Mismatches: 31
Query Match: 9.1% Indels: 18
DB: 7 Gaps: 4

US-08-817-997-2_COPY_36_229 (1-194) x US-10-802-796-496 (1-420)
QY 94 CysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAla 113
Db 146 TGC CGG GGC CAC GAG GTT GCT CCG CGG TACT CCG CAG GGT GCG CGT GAT CNA CAT C 205
QY 114 AlaValSer-----GluLeuSerGlyAlaValLys 123
Db 206 GTC ACC GCG CAC CAC TAC TCG GGT TCC AAG ACC CCG TGT TCG CGC CCG CAG CGG C 265
QY 124 GluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGly 143
Db 266 GAT CAT CAC TCG CGG CAG TCG CCG CTT GTT TCG G-----AAT CCT CGG CGC GCG TGG C 316
QY 144 -----IleAlaAsnTyrProArg-----GluArgThrLysValPheCysAsnVal 158
Db 317 GGC TGT GAT GAG CGC CCG TCA TCG GGT CCA AACC CAT CNA CCT CTG CAACAAC 376
QY 159 GlyAspAlaValCysThr 164
Db 377 GGC GAC CCG CAG ATT GTT TCG 394

RESULT 5
US-11-052-554A-519/c
; Sequence 519, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 519
; LENGTH: 5706
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-519

Alignment Scores:
Pred. No.: 55.8 Length: 5706
Score: 89.00 Matches: 43
Percent Similarity: 41.7% Conservative: 10
Best Local Similarity: 33.9% Mismatches: 62
Query Match: 8.9% Indels: 12
DB: 8 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-11-052-554A-519 (1-5706)

Qy 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu-----IlePheAla 25
Db 3852 GGCAGCGAATCCGGCGTTCGCCCGCTCCCGCGCATGCCGCGCTTGGCCGCGCATCCGCC 3793

Qy 26 ArgGlySerThrGluProGlyAsnMetGly---IleThrValGlyProAlaLeuAlaAsn 44
Db 3792 GTCGGGTCGCCGATCAGGTCCCGGGGGCGGTCAACACCGCCCGCGGTGGCGCC 3733

Qy 45 GlyLeuGluSerHisLeuArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAla 64
Db 3732 GCGCCCGCGCGCGCGCTTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3673

Qy 65 AlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLys 84
Db 3672 GCGTTGGCGGCC-----GTCAAGCGCGAGAGCGCCAGGCC-----GAGACCGGTGGC 3625

Qy 85 ArgLeuPheAlaAlaAsnGlnLysCysProAsnThrProVal---ValAlaGlyGly 103
Db 3624 TCCTCGCGCGCGTACCC-----GCCAACACCGCGCTTCCCGCGCGCGCGCG 3577

Qy 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 3576 CTTACCGCGCGCGCGCGCGAAGCGCGCGCCACCACCGAGCGCGCATCGCGCGGTCCCC 3517

Qy 124 GluGlnValLysGlyValAla 130
Db 3516 GCGCGTGGCGCGCGAGCGCGCC 3496

RESULT 6
US-10-838-616-17/c
; Sequence 17, Application US/10838616
; Publication No. US20060008874A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: CREELMAN, Robert A.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
; FILE REFERENCE: MBI-0069CIP
; CURRENT APPLICATION NUMBER: US/10/838,616
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
```

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; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/685,922
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 09/810,836
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: G3451 Predicted polypeptide sequence is orthologous to G867, G9,
US-10-838-616-17

Alignment Scores:
Pred. No.: 11.9 Length: 1253
Score: 87.00 Matches: 51
Percent Similarity: 32.9% Conservative: 24
Best Local Similarity: 22.4% Mismatches: 86
Query Match: 8.7% Indels: 67
DB: 6 Gaps: 9

US-08-817-997-2_COPY_36_229 (1-194) x US-10-838-616-17 (1-1253)

Qy 11 SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySer-ThrG1 30
Db 1180 TCTTCTCTCCATTGCCATGCGACCCACTTGCATTTATTGTATTGCAACAATAGTATCTGA 1121

Qy 30 uProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisI1 50
Db 1120 ACCGGGTAGTTTCAAAATG-----TTAAACCCCAAGAG 1088

Qy 50 eArgAsnIleTrpIle-----GlnGlyValGlyGlyProTyrAspAla---AlaIe 66
Db 1087 CCGAACCATCTGGATCGGTTTCGACACCGGTCCGACCGGTCCGACCAACGCGACCTCGTT 1028

Qy 66 uAlaThrAsnPheLeu-----ProArgGlyTh 75
Db 1027 GTTAACAACATCTCTCTTCCAATCGATGAAGTGTCTTCCGCTCCAGTGGACCG 968

Qy 75 rSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysePr 95
Db 967 GTGAACAACAAACCGGTGTCACCGCTTTCAGATTCTTCTCTTAACGAACCGGCTCCAACC 908

Qy 95 o----- 95
Db 907 TTTGTTTAAGACGTAACCTCTGGCTACTGTTCCAATACGAGTAACGAAACCGCACACTTT 848

Qy 96 -----AsnThrProValValAlaGlyGlyTyrSerGlnG1 107
Db 847 CCCTCCAACGTTCTCGAAGTTCAACAAACCGCTTCCGCCCGGTCCGCGTCCAC 788

Qy 107 yAlaAlaLeuIleAlaAlaValSer---GluLeuSerGlyAlaValLysGluGlnVa 126
Db 787 CGCGCTCTGCTCGCGCTTAACCGCTTAGAGCTCTGTAAACGGA-----AAGTG 737

Qy 126 lLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAs 146
```

Db 736 CTCTCCGCGTCTGGTATCACCAACGGTTC-----AA 698
Qy 146 nTyrProArgGluArgThrIlysValPheCysAsnValGlyAspAlaValCysThrGlyTh 166
Db 697 TTTCCTCA-----ACGTGCTCGCGGTAAACAGCCTTCTCGAATAGTCTCAGCTGC 647
Qy 166 rLeullelleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAa 186
Db 646 CTTAGTAAACACGCGCGGAAATTGAGTTTGGTGGTGGCGCGCGGAGCTCGCGC 587
Qy 186 qPheLeuArgAspArgIleArg 193
Db 586 CCGGACGACGCGCGGTGCGC 565

RESULT 7

US-10-522-037-2/c
; Sequence 2, Application US/10522037
; Publication No. US20050282166A1
; GENERAL INFORMATION:
; APPLICANT: LIBRAGEN
; TITLE OF INVENTION: Method for the expression of unknown environmental DNA into adap
; TITLE OF INVENTION: cells.
; FILE REFERENCE: B0149W0
; CURRENT APPLICATION NUMBER: US/10/522,037
; CURRENT FILING DATE: 2005-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 37507
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of clone F83-135.
US-10-522-037-2

Alignment Scores:
Pred. No.: 2,33e+03 Length: 37507
Score: 84.50 Matches: 51
Percent Similarity: 42.0% Conservative: 22
Best Local Similarity: 29.3% Mismatches: 68
Query Match: 8.5% Indels: 34
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-522-037-2 (1-37507)

Qy 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
Db 21962 GCGCGGCGCGCTCGATGTCGGAGTGGCGCGCTTCATCGCCTCGCGCTGCA--- 21906
Qy 45 GlyLeuGluSerHisIleArgAsnIleTIpIleGlnGlyValGlyGlyProTyrAspAla 64
Db 21905 -----CCGCTTCGCGGTGACGAGGCGCGCTGC-GTGCGCGCC 21865
Qy 65 AlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLys 84
Db 21864 GCGCGTCCGCGCGGTGATCCCGCGCGC---TCTCGCGCAACATTCGTGCTCG--- 21811
Qy 85 ArgLeuPheAlaLeuAlaGlnLysCysProAsn-----ThrPro-ValValAlaGl 102
Db 21810 -----GCGAATCGCTGATGCGGTGCGCGCTCGCGCTCGCGCTCGCGCGC 21766
Qy 102 yGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVa 122
Db 21765 AGGTTTCGCGCGAGGTGCGCACCGCGGTGTCGCGCGGTTCGCGAGCGTCCGCGCA-- 21708
Qy 122 lLysGluGlnValIysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGl 142
Db 21707 -----CGCGCGGAGCGGAACCTGTTGTGGCGCGCTCCCGCTCTCCGGGGCGACG 21655
Qy 142 yGlyIleAlaAsnTyrProArgGluArgThrIlysValPheCysAsnValGlyAspAlaVa 162
Db 21654 CAAGCGCGAGGTGCGCGCGCTCGA----- 21627

Qy 162 lCyThrGlyThrLeullelleThrProAla-HisLeuSerTyrThrIleGluAlaArgG 182
Db 21626 -TGC CGCGCGCTTCGTTCCTGAGCCCACTACACGCGCGCGCTCGCGCTCGCGCGC 21568
Qy 182 lYGuAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 21567 GCGAGCTGCG---ATGCTGCGCGATTCGCTCGCGGCC 21533

RESULT 8

US-10-467-657-2927
; Sequence 2927, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2927
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2927

Alignment Scores:
Pred. No.: 8.51 Length: 414
Score: 82.50 Matches: 36
Percent Similarity: 44.6% Conservative: 18
Best Local Similarity: 29.8% Mismatches: 36
Query Match: 8.3% Indels: 31
DB: 7 Gaps: 8

US-08-817-997-2_COPY_36_229 (1-194) x US-10-467-657-2927 (1-414)

Qy 27 GlySerThrGluProGlyAsnMetGlyIleThrValGly----- 39
Db 55 GGTTCCTCAAAGGCGGGAATGCTGTTCTTCTTGTGCGTGGTCAGATTCTTGTGCGCTCC 114
Qy 40 -----ProAla---LeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTIpIleGln 56
Db 115 GGGCAACCGACCGGAAATTGAAACCGCTGCATCCAGCGCTCCGGAATATATATGCTTCAG 174
Qy 57 GlyVal-----GlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuPro 72
Db 175 GTTTTCATGTCGCCAAGATGAGCGGTACATTGCT-----GTAACTGCTTCCTG--- 225
Qy 73 ArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGln 92
Db 226 -----CAGACGGCATCGGTGTTGTTTCAGGGCTTCGCGCTG-----GATGTC 267
Qy 93 LysCysProAsnThrProValValAlaGlyTyrSerGlnGlyAlaAlaLeuIleAla 112
Db 268 GAATGCCACACTTTCCTCCCTGTTGCTGCGTGGTGTGCGAGGAAAGGGTGTGCGTGC 327
Qy 113 AlaAlaValSerGluLeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPhe 132
Db 328 GTTGCC-----GGCGGTGCGCTCCAGCGC-----ATTGCGGCTTC 363
Qy 133 Gly 133
Db 364 GGG 366

RESULT 9

US-10-750-185-27797/c

; Sequence 27797, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10750,185
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27797
 ; LENGTH: 1093
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880669084
 ; US-10-750-185-27797

Alignment Scores:
 Pred. No.: 36.3 Length: 1093
 Score: 82.00 Matches: 45
 Percent Similarity: 40.9% Conservative: 27
 Best Local Similarity: 25.6% Mismatches: 66
 Query Match: 8.2% Indels: 38
 DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-750-185-27797 (1-1093)

```

Qy 35 GlyIleThrValGlyProAlaLeuAla---AsnGlyLeuGluSerHisIleArgAsn--- 52
Db 579 GGGACTGTCTCGTGGTCCCTCCCTGGCGGCTGAGGAGGCTGAGCTGAGAGGCT 520
Qy 53 -----IleTrrIleGlnGlyValGlyGlyPro-TyrAspAlaAlaLeuAlaTh 68
Db 519 CCCACGTGCTGGAGTGGCCCCAAGGCTGAGGAGCCTTGCCACTGCCGCCACCCTC 460
Qy 68 rAnPheLeu---ProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPh 87
Db 459 CCAGTTCTTTCAGCCCTGTGGCGGGCCCGAGCCCACTTGAGGAGGCTAGGAGCTCT 400
Qy 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnG 107
Db 399 GGGTTGGTGGGACAGAG-----GTGGTCTGTGGC-----CAGGG 367
Qy 107 yAlaAlaLeuIleAlaAlaValSerGluLeuSerGly----- 120
Db 366 GGCTGTCTGTGGCGGAGACTGTGGCCAGCTTCCAGACGCCAAGCTGTTCTGTCCAGTT 307
Qy 121 ----AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuG 139
Db 306 GTTGGCTGACGCTGTGGCAGCTAGGAGTCTGATGCCATCCAGCAGGAGAGCAGC 247
Qy 139 nAnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCys----- 156
Db 246 ATCTGTAGTTCGACTCCGGGACTTCCAGAAATGAAGGAAAGCATGTGCTTCTTGTG 187
Qy 157 -----AsnValGlyAspAlaValCysThrGlyThrLe 167
Db 186 GAGCCTTGTCCCTTTCCTGTGATGGGGTAAGTGGGTTCAGTTCATTCCTCAAAATATTTT 127
Qy 167 uIle-IleThrProAlaHisLeuSerTyrThrIleGluAlaArg 181
Db 126 AGTGTCTATTCCCGAGTACTGAAACACACTTGAGGGGTAGA 83

```

RESULT 10
 US-10-750-623-27797/c
 ; Sequence 27797, Application US/10750623

; Publication No. US20050287531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-1
 ; CURRENT APPLICATION NUMBER: US/10750,623
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27797
 ; LENGTH: 1093
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880669084
 ; US-10-750-623-27797

Alignment Scores:
 Pred. No.: 36.3 Length: 1093
 Score: 82.00 Matches: 45
 Percent Similarity: 40.9% Conservative: 27
 Best Local Similarity: 25.6% Mismatches: 66
 Query Match: 8.2% Indels: 38
 DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-750-623-27797 (1-1093)

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Qy 35 GlyIleThrValGlyProAlaLeuAla---AsnGlyLeuGluSerHisIleArgAsn--- 52
Db 579 GGGACTGTCTCGTGGTCCCTCCCTGGCGGCTGAGGAGGCTGAGCTGAGAGGCT 520
Qy 53 -----IleTrrIleGlnGlyValGlyGlyPro-TyrAspAlaAlaLeuAlaTh 68
Db 519 CCCACGTGCTGGAGTGGCCCCAAGGCTGAGGAGCCTTGCCACTGCCGCCACCCTC 460
Qy 68 rAnPheLeu---ProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPh 87
Db 459 CCAGTTCTTTCAGCCCTGTGGCGGGCCCGAGCCCACTTGAGGAGGCTAGGAGCTCT 400
Qy 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnG 107
Db 399 GGGTTGGTGGGACAGAG-----GTGGTCTGTGGC-----CAGGG 367
Qy 107 yAlaAlaLeuIleAlaAlaValSerGluLeuSerGly----- 120
Db 366 GGCTGTCTGTGGCGGAGACTGTGGCCAGCTTCCAGACGCCAAGCTGTTCTGTCCAGTT 307
Qy 121 ----AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuG 139
Db 306 GTTGGCTGACGCTGTGGCAGCTAGGAGTCTGATGCCATCCAGCAGGAGAGCAGC 247
Qy 139 nAnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCys----- 156
Db 246 ATCTGTAGTTCGACTCCGGGACTTCCAGAAATGAAGGAAAGCATGTGCTTCTTGTG 187
Qy 157 -----AsnValGlyAspAlaValCysThrGlyThrLe 167
Db 186 GAGCCTTGTCCCTTTCCTGTGATGGGGTAAGTGGGTTCAGTTCATTCCTCAAAATATTTT 127
Qy 167 uIle-IleThrProAlaHisLeuSerTyrThrIleGluAlaArg 181
Db 126 AGTGTCTATTCCCGAGTACTGAAACACACTTGAGGGGTAGA 83

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RESULT 11
 US-11-117-187-196/c
 ; Sequence 196, Application US/11117187
 ; Publication No. US20050266560A1

```
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPEHAEVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 196
; LENGTH: 96988
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-196

Alignment Scores:
Pred. No.: 2.11e+04 Length: 96988
Score: 81.00 Matches: 25
Percent Similarity: 47.9% Conservatives: 10
Best Local Similarity: 34.2% Mismatches: 20
Query Match: 8.1% Indels: 18
DB: 8 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x US-11-117-187-196 (1-96988)

Qy 47 GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyr----- 62
Db 80971 GAGAGCTAACTCAACATCTTCTACAAAGGATAGACAGCCATACCAATCAACTT 80912
Qy 63 AspAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle----- 80
Db 80911 GATGACGAAGCTCCTGTAATTCATGACGAAGAACCACTAGTGAAGCATTAATCTATC 80852
Qy 81 -----AspGluGlyLysArgLeuPheAla 88
Db 80851 ACCAATGCTTTAACTGCTCATTGCGAGTAGTAATTGACAAAGAACGAAGATTTCAGCT 80792
Qy 89 LeuAlaAsnGlnLysCysProAsnThrProValValala 101
Db 80791 GAGAAAGCTACCAAGTGAAGAGAGACTCATGTTTCAGCA 80753

RESULT 12
US-11-121-086-15/c
; Sequence 15, Application US/11/121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 169047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-15

Alignment Scores:
Pred. No.: 5.13e+04 Length: 169047
Score: 80.50 Matches: 35
Percent Similarity: 47.2% Conservatives: 16
Best Local Similarity: 32.4% Mismatches: 38
Query Match: 8.1% Indels: 20
DB: 8 Gaps: 7
```

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US-08-817-997-2_COPY_36_229 (1-194) x US-11-121-086-15 (1-169047)

Qy 4 AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIle 23
Db 58404 GCCACAAAGACAGGGCTTCC-ACTGGCACCTCTCACCCTCCCTGCTGCTCCCTCTCG 58346
Qy 24 PheAlaArgGlySer---ThrGluProGlyAsnMetGly-----Ile 36
Db 58345 GGTGCACCTGGCTCTTTGGCCCTCTCTGGAGGTAGGATGGCCCTTCGGGGCTGTGTGTG 58286
Qy 37 ThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIle-----Tip 54
Db 58285 CTCITGGGACAGCGGCTCTGCAGATCCCTCGAGCCACACACACCGGCACTCTGCGAGTGG 58226
Qy 55 IleGlnGlyVal-----GlyGlyProTyrAspAlaLeuAlaThrAsnPhe 70
Db 58225 GAGCTTGGCAGCCCGCCAGCACAGGTACACCTACCATGTGTCTCTAGCAGAG----- 58172
Qy 71 LeuProArgGlyThrSer---GlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeu 89
Db 58171 CTCCCTACTGGGAGCATGTAAAGGAAATAACAACCAAGGC-----TTTGCCATA 58121
Qy 90 AlaAsnGlnLysCysProAsnThr 97
Db 58120 AGCAATGTAAATGTCCAACTCC 58097

RESULT 13
US-10-838-616-25/c
; Sequence 25, Application US/10838616
; Publication No. US2006000874A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: CREELMAN, Robert A.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
; FILE REFERENCE: MBI-0069CIP
; CURRENT APPLICATION NUMBER: US/10/838,616
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/685,922
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 09/810,836
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: G3454 Predicted polypeptide sequence is orthologous to G867
US-10-838-616-25
```

Alignment Scores: 68.4 Length: 1188
Pred. No.: 80.00 Matches: 50
Score: 31.7% Conservative: 23
Percent Similarity: 21.7% Mismatches: 86
Best Local Similarity: 8.0% Indels: 71
Query Match: 6 Gaps: 9
DB:

US-08-817-997-2_COPY_36_229 (1-194) x US-10-838-616-25 (1-1188)

Qy 11 SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySer-ThrG1 30
Db 1128 TCTTCTCTGTCATGAGCACCACCTTGCATTATTGTTATGCAACAATAGTATCTGA 1069
Qy 30 uProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHis11 50
Db 1068 ACCGGGTAGTTTCAAAATG-----TTAACCACCAAGAG 1036
Qy 50 eArgAsnIleTrpIle-----GlnGlyValGlyGlyProTyrAspAla---AlaLe 66
Db 1035 CCGAACCATCTGATCGGTTTCGACACCGGTCGACCGGTCGGAACACGACGACCTCGTT 976
Qy 66 uAlaThrAsnPheLeu-----ProArgGlyTh 75
Db 975 GTTAACAACATCTCTCGTCTTCAATCGATGTAAAGCTGTTGTCGGTCCAGTGGACCG 916
Qy 75 rSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysPr 95
Db 915 GTGAAAAACAACCGTGTACACGCTTCAGATTCCTCTTAACGAACCGGCTCCAAACC 856
Qy 95 O----- 95
Db 855 TTTGGTTAAGACGTAACCTCTGCTACTGTTTCAATACGAGTAACGAAACCGCACACTTT 796
Qy 96 -----AenThrProValValAlaGlyGlyTyrSerGlnG1 107
Db 795 CCCTCCAAACGCTCTTCAAGATTCAACAAACGCGCTTCGCGCGCTCGCGCTCGAC 736
Qy 107 yAlaAlaLeuIleAlaAlaValSer---GluLeuSerGlyAlaValLysGluGlnVa 126
Db 735 CGCGCGTATCTGTCGCGCTAACCGCTTAGAGCTCTGTAAACGGA-----AAAGTG 685
Qy 126 lLysGlyValAlaLeuPheGlyTyrThrGln-----AsnLeuGlnAsnArgGlyGly11 144
Db 684 CTTCTCGCGTGTGCTTTCGATATCACCACAAACGCTTCAATTCCAAACGCTCGCTCGG 625
Qy 144 eAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysTh 164
Db 624 AACAGCTTTCTCGAATAGC-----TGCTC 601
Qy 164 rGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAl 184
Db 600 ACCTGATCATAGTAAGACACGCGCGGAAATTTAGTCTGCGGTGCGGACGCGCGGAGCC 541
Qy 184 aAlaArgPheLeuArgAspArgIleArg 193
Db 540 TCAGCGCGCGACGACGCGCGGTTGCGC 513

RESULT 14
US-11-052-554A-522/c
; Sequence 522, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIOR FILING DATE: 2005-02-07
; PRIOR FILING DATE: 2004-07-20
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004

; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 4146
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-522

Alignment Scores: 427 Length: 4146
Pred. No.: 79.50 Matches: 47
Score: 35.4% Conservative: 17
Percent Similarity: 26.0% Mismatches: 66
Best Local Similarity: 8.0% Indels: 51
Query Match: 8 Gaps: 10
DB:

US-08-817-997-2_COPY_36_229 (1-194) x US-11-052-554A-522 (1-4146)

Qy 2 LeuGlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIle 21
Db 2235 CTGGCCGCGCGCCCGCGCATTCGCCCTGCGCGCGCGCGCCACCGCTCGCGCGCTC 2176
Qy 22 LeuIlePheAlaArgGlySerThrGluProGlyAsnMet-----Gly 35
Db 2175 TCCACCTTTGGCGCGCGTGC-----CCCGCAGGCTCTGTGCCAGTCCCGGTATGCC 2122
Qy 36 IleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrpIle 55
Db 2121 GTTCCGCGCGCGCC-----GCCAATGCTCCCGCACCGCGCTCACCGCCATTACCACC 2068
Qy 56 Gln-----GlyValGlyGlyProTyrAspAlaLeuAlaLeuAlaThrAsn 69
Db 2067 GCTGCGCGCGGTTTCGCCATTGCGCGCGCGCGCGCTACGCGCGCTTGCACCGCGC 2008
Qy 70 PheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeu 89
Db 2007 -----GCCCGCGCTGAAGCGCGC-----TTGCGCGCTC 1981
Qy 90 AlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAla 109
Db 1980 CAC-----CCCAAAAGTTGCCGCTGTTGCC-----GGTGCCAGC 1948
Qy 110 LeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnValLysGlyVal 129
Db 1947 CTTGCGCGCGCGCGGTTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1888
Qy 130 AlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyIleAlaAsnTyrProArg 149
Db 1887 GCTGCC-----CGCGGTGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGC 1855
Qy 150 GluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIle 169
Db 1854 -----TGC 1813
Qy 170 Thr 170
Db 1812 ACC 1810

RESULT 15
US-10-802-796-75
; Sequence 75, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESEN-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000

; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 75
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-75

Alignment Scores:
Pred. No.: 23.3 Length: 445
Score: 79.00 Matches: 35
Percent Similarity: 45.9% Conservative: 10
Best Local Similarity: 35.7% Mismatches: 34
Query Match: 7.9% Indels: 21
DB: 7 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-802-796-75 (1-445)

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QY 94 CysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAla-----Leu 110
Db 153 TGCCGGGCCACGAGGTGTGCTCGCGGCTACTCCAGGGTGGCGCGTGATCGACATC 212
QY 111 IleAlaAlaAla-----ValSerGluLeuSerGlyAlaValLys 123
Db 213 GTCACGCGCGCACCACTGCCCGCGCTCGGGTTACGCGAGCGGTTCGCCCGCGCAGCGGAC 272
QY 124 GluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGly 143
Db 273 GATCATATCGCCGCGATCGCCCTGTTCGG-----AATCCCTCGGGCGCGCTGGC 323
QY 144 -----IleAlaAsnTyrProArgGluArgThrLys-----ValPheCysAsnVal 158
Db 324 GGGCTGATGAGCGCCCTGACCCCTCAATTCCGGTCCAGAACATCAACCTCTGCACCAAC 383
QY 159 GlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyr 176
Db 384 GCGGACCC-ATTGTTC-GGACGCGCAACCGGTGGCA---ACGCACCTAAGCTAC 432
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Search completed: February 5, 2006, 00:35:34
Job time : 268 secs